

Db 61 RFVVDMLHHCIAKRWIAQRGQVVAALNLGNGPLNVLVGLGVLLGQFVVRERFEKS 116

RESULT 14

ID AAB35127 standard; protein; 52 AA.

XX AAB35127;

XX 03-APR-2001 (first entry)

DE Mammalian Bak alpha-5 and alpha-6 helices.

XX Mammal; Bak; apoptosis modulator; BCL-2.

XX Mammalia.

XX US6165732-A.

XX 26-DEC-2000.

XX 31-JUL-1998; 98US-0127048.

XX 14-OCT-1997; 97US-0061823.

XX (UNIW) UNIV WASHINGTON.

XX Korsmeyer SJ, Schlesinger PH;

XX WPI; 2001-101692/11.

XX Identifying apoptosis-modulating compounds by contacting the compound

XX with lipid bilayer containing an ion channel formed by anti-apoptotic

XX polypeptide of Bcl-2 family and determining ion selectivity of the

XX channel -

XX Example 7; Fig 7; 34pp; English.

XX The present invention describes a method for identifying modulators of

XX apoptosis which involves contacting a compound of interest with a lipid

XX bilayer comprising a K⁺ or Cl⁻ selective channel. This channel is a

XX member of the BCL-2 family. Apoptosis modulators are also provided,

XX including Bcl-2deltaTAM and BaxdeltaTAM.

XX Sequence 52 AA;

XX Query Match 25.7%; Score 284; DB 22; Length 52;

XX Best Local Similarity 100.0%; Pred. No. 1.1e-23;

XX Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 123 INMGVVALLGFGYRLALHYOHGLTGFLGQVTRFVVDMLHHCIAKRWIAQR 174

XX 1 INMGVVALLGFGYRLALHYOHGLTGFLGQVTRFVVDMLHHCIAKRWIAQR 52

XX Db 1 INMGVVALLGFGYRLALHYOHGLTGFLGQVTRFVVDMLHHCIAKRWIAQR 52

XX RESULT 15

XX AAU76550

XX ID AAU76550 standard; Protein; 52 AA.

XX AAU76550;

XX 08-MAY-2002 (first entry)

DE Murine Bak peptide containing helices alpha-5 and alpha-6.

XX Mouse; Bak; alpha-5 helix; alpha-6 helix; BCL-2; apoptosis modulation;

XX neoplasia; Epstein-Barr virus; African swine fever virus; adenovirus;

XX lymphoproliferative condition; cancer; arthritis; Crohn's disease; wound;

XX inflammation; autoimmune disease; immunodeficiency disease; senescence;

XX neurodegenerative disease; ischemic cell death; reperfusion cell death;

XX infertility; apoptosis-promoting peptide.

XX Mus sp.

XX PN WO200205835-A2.

XX PD 24-JAN-2002.

XX 25-JUN-2001; 2001WO-US20169.

XX 17-JUL-2000; 2000US-0617878.

XX (UNIW) UNIV WASHINGTON.

XX Korsmeyer SJ, Schlesinger PH;

XX WPI; 2002-179747/23.

XX Identifying apoptosis modulating compounds for treating e.g. cancer,

XX comprises contacting a lipid membrane with a pore-forming BCL-2 member

XX and test compound, and determining if formation of large pores in the

XX membrane is regulated -

XX Example 7; Fig 7; 70pp; English.

XX The invention relates to a method for identifying apoptosis modulating

XX compounds, involving contacting a lipid membrane with a pore-forming

XX pro-apoptotic BCL-2 family member and a test compound, and determining

XX whether the compound regulates formation of large pores in the lipid

XX membrane. An increase in the number of large pores in the lipid membrane

XX indicates that the compound is an apoptosis promoter and a decrease in

XX the number of large pores indicates that it is an apoptosis inhibitor.

XX Apoptosis modulating compounds are useful for inducing or inhibiting

XX apoptosis in a cell, to treat a patient having a condition mediated by

XX excessive down-regulation of apoptosis (such as neoplasias, diseases

XX caused by Epstein-Barr virus, African swine fever virus and adenovirus,

XX lymphoproliferative conditions, cancer, arthritis, Crohn's disease,

XX inflammation and autoimmune diseases), or excessive apoptosis (such as

XX immunodeficiency diseases, senescence, neurodegenerative diseases,

XX ischemic and reperfusion cell death, infertility and wounds. This

XX sequence represents a mouse Bak apoptosis-promoting peptide containing

XX the alpha-5 and alpha-6 helices, used in the methods of the invention.

XX Sequence 52 AA;

XX Query Match 25.7%; Score 284; DB 23; Length 52;

XX Best Local Similarity 100.0%; Pred. No. 1.1e-23;

XX Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 123 INMGVVALLGFGYRLALHYOHGLTGFLGQVTRFVVDMLHHCIAKRWIAQR 174

XX 1 INMGVVALLGFGYRLALHYOHGLTGFLGQVTRFVVDMLHHCIAKRWIAQR 52

XX Db 1 INMGVVALLGFGYRLALHYOHGLTGFLGQVTRFVVDMLHHCIAKRWIAQR 52

XX Search completed: March 27, 2003, 10:52:30

XX Job time : 75 secs

SQ Sequence 117 AA;

Query Match 56.7%; Score 625; DB 19; Length 117;

Best Local Similarity 100.0%; Pred. No. 1e-60;

Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 71 MGQVGRQALAIIGDDINRRYDSFQTMLOHLPQTAENAYEFTKIATSLFESGIMNGRYVA 130
 |||||||
 DB 1 MGQVGRQALAIIGDDINRRYDSFQTMLOHLPQTAENAYEFTKIATSLFESGIMNGRYVA 60

QY 131 LIGFGYRLALHYQHGLTGFGLGQVTRFYVDPEMLHHCIARWIAQRGWAALNLGNP 187
 |||||||
 DB 61 LIGFGYRLALHYQHGLTGFGLGQVTRFYVDPEMLHHCIARWIAQRGWAALNLGNP 117

RESULT 12

AAR77881 AAR77881 standard; Protein; 116 AA.

AAR77881;

DT 21-NOV-1995 (first entry)

DE Human Cdn-1(96-211).

XX Cdn-1; apoptosis modulator; adoptive immunotherapy; therapy; HIV;
 KW autoimmune disease; reperfusion injury; hepatitis, osteoporosis;
 KW shock; lymphoma; eczema.

OS Homo sapiens.

PN WO9515084-A.

PD 08-JUN-1995.

PF 30-NOV-1994; 94WO-US13930.

PR 07-OCT-1994; 94US-0320157.

PR 30-NOV-1993; 93US-0160067.

PA (LXRB-) LXR BIOTECHNOLOGY INC.

PI Barr PJ, Kiefer MC;

DR WPI; 1995-215106/28.

XX New nucleic acid sequences encoding Cdn apoptosis modulators - and
 PT related vectors, transformed cells, proteins and antibodies, useful
 PT or diagnosis and treatment e.g. of HIV infection, reperfusion injury
 PT etc.

PS Disclosure; Fig. 11; 66pp; English.

XX Expression of Cdn-1 in WI-L2 lymphoblastoid cells resulted in
 CC increased cell survival in response to anti-Fas-mediated apoptosis.
 CC Truncated Cdn-1 derivatives given in AAR77879-81 were used to
 CC test the effects of deleting the N-terminal sequences of Cdn-1
 CC on this activity.

SQ Sequence 116 AA;

Query Match 55.2%; Score 609; DB 16; Length 116;

Best Local Similarity 100.0%; Pred. No. 5.8e-59;

Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 96 MLOHLOPTAENAYEFTKIATSLFESGIMNGRYVALLGFGYRLALHYQHGLTGFGLGQVT 155
 |||||||

DB 1 MLOHLOPTAENAYEFTKIATSLFESGIMNGRYVALLGFGYRLALHYQHGLTGFGLGQVT 60
 |||||||

QY 156 RFVVDPEMLHHCIARWIAQRGWAALNLGNPILNVLVGLGVVLLGQFVYRRFFKS 211
 |||||||

DB 61 RFVVDPEMLHHCIARWIAQRGWAALNLGNPILNVLVGLGVVLLGQFVYRRFFKS 116
 |||||||

RESULT 13

AAW79536 AAW79536 standard; Protein; 116 AA.

AAW79536;

DT 11-JAN-1999 (first entry)

DE Truncated Bak polypeptide Bak-delta3.

XX Bak; bak binding protein; BBP; bbpbd-1; bbpbd-2; Bcl-2; apoptosis;
 KW cell death; cancer; lymphoma; neurodegeneration; heart disease;
 KW cell proliferation; infection; human; therapy; diagnosis.

OS Homo sapiens.

FH Key Location/Qualifiers

FT Peptide 8..31 /label= BBPBD-1

FT Peptide 43..61 /note= "Claim 36"

FT Peptide /label= BBPBD-2

FT Peptide /note= "Claim 62"

PN WO9841626-A1.

PD 24-SEP-1998.

PE 03-MAR-1998; 98WO-US04079.

PR 09-JAN-1998; 98US-0071097.

PR 20-MAR-1997; 97US-0041328.

PA (LXRB-) LXR BIOTECHNOLOGY INC.

PI Barr PJ, Fitzpatrick PA, Gibson HL, Kiefer MC;

DR WPI; 1998-521220/44.

XX New Bak-binding protein and related nucleic acid, vectors,
 PT transformed cells and antibodies - are useful for modulation of
 PT apoptosis in cancer, neuro-degeneration etc., also peptide fragments
 PT of Bak that interact with the protein

PS Example 5; Page 54; 77pp; English.

XX This is the amino acid sequence of Bak-delta3, an N-terminal
 CC deletion mutant of Bak (see AAW79534) comprising amino acids 96-210
 CC of the full-length protein. PCR amplified Bak-delta3 was subcloned
 CC into vector pBluebacII and used in experiments to determine
 CC the interaction between Bak and a novel Bak binding protein (BBP,
 CC see AAW79537). The results indicated that Bak-delta3 is capable
 CC of interaction with loop 1 of BBP but not with the hydrophilic
 CC region represented by BBP loop 2. Bak-delta3 includes the claimed
 CC BBP binding domains of BBP but that are suggested to be important death
 CC domains of Bak. The invention relates to BBP, the gene encoding
 CC BBP (see AAW61499), methods for detecting substances that alter the
 CC specific binding between Bak and BBP, as well as diagnostic and
 CC therapeutic methods utilizing BBP.

SQ Sequence 116 AA;

Query Match 55.2%; Score 609; DB 19; Length 116;

Best Local Similarity 100.0%; Pred. No. 5.8e-59;

Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 96 MLOHLOPTAENAYEFTKIATSLFESGIMNGRYVALLGFGYRLALHYQHGLTGFGLGQVT 155
 |||||||

DB 1 MLOHLOPTAENAYEFTKIATSLFESGIMNGRYVALLGFGYRLALHYQHGLTGFGLGQVT 60
 |||||||

QY 156 RFVVDPEMLHHCIARWIAQRGWAALNLGNPILNVLVGLGVVLLGQFVYRRFFKS 211
 |||||||

DB 61 RFVVDPEMLHHCIARWIAQRGWAALNLGNPILNVLVGLGVVLLGQFVYRRFFKS 116
 |||||||

XX New nucleic acid sequences encoding Cdn apoptosis modulators - and
 PT related vectors, transformed cells, proteins and antibodies, useful
 PT or diagnosis and treatment e.g. of HIV infection, reperfusion injury
 PT etc.
 XX
 PS Disclosure; Fig.11; 66pp; English.
 XX
 CC Expression of Cdn-1 in WI-L2 lymphoblastoid cells resulted in
 CC increased cell survival in response to anti-Fas-mediated apoptosis.
 CC Deletion of the N-terminal 59 amino acids of Cdn-1 only slightly
 CC decreased this activity, suggesting that small, truncated Cdn-1
 CC molecules may be potent therapeutics.
 CC
 SQ Sequence 152 AA:
 Query Match 71.7%; Score 791; DB 16; Length 152;
 Best Local Similarity 100.0%; Pred. No. 7,8e-79;
 Matches 152; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 60 MVTLPDPSSSTMGQVGRQALITGDDINRRYSEFQTMLOHLPATNAVEYFTKIATSLF 119
 DB 1 MVTLPDPSSSTMGQVGRQALITGDDINRRYSEFQTMLOHLPATNAVEYFTKIATSLF 60
 QY 120 ESGINMGVVALLGFGYRLAHYOHGTLGQVTRFVVDMLHRCIARMTAORGGWVA 179
 DB 61 ESGINMGVVALLGFGYRLAHYOHGTLGQVTRFVVDMLHRCIARMTAORGGWVA 120
 QY 180 ALNIGNGPIINVLVLGVLLGQFVVRPFKS 211
 DB 121 ALNIGNGPIINVLVLGVLLGQFVVRPFKS 152
 RESULT 10
 AAR77880
 ID AAR77880 standard; Protein; 141 AA.
 XX
 AC AAR77880;
 XX
 DT 21-NOV-1995 (first entry)
 XX
 DE Human Cdn-1(71-211).
 XX
 KW Cdn-1; apoptosis modulator; adoptive immunotherapy; therapy; HIV;
 KW autoimmune disease; reperfusion injury; hepatitis, osteoporosis;
 KW shock; lymphoma; eczema.
 XX
 OS Homo sapiens.
 XX
 PN WO9515084-A.
 XX
 PD 08-JUN-1995.
 XX
 PF 30-NOV-1994; 94WO-US13930.
 XX
 PR 07-OCT-1994; 94US-0320157.
 PR 30-NOV-1993; 93US-0160067.
 XX
 PA (LXRB-) LXR BIOTECHNOLOGY INC.
 XX
 PI Barr PJ, Kiefer MC;
 XX
 DR WPI; 1995-215106/28.
 XX
 PT New nucleic acid sequences encoding Cdn apoptosis modulators - and
 PT related vectors, transformed cells, proteins and antibodies, useful
 PT or diagnosis and treatment e.g. of HIV infection, reperfusion injury
 PT etc.
 XX
 PS Disclosure; Fig.11; 66pp; English.
 PS
 CC Expression of Cdn-1 in WI-L2 lymphoblastoid cells resulted in
 CC increased cell survival in response to anti-Fas-mediated apoptosis.
 CC

CC Deletion of the N-terminal 70 amino acids of Cdn-1 improved this
 CC activity, suggesting that small, truncated Cdn-1 molecules may be
 CC potent therapeutics.
 CC
 SQ Sequence 141 AA:
 Query Match 66.8%; Score 737; DB 16; Length 141;
 Best Local Similarity 100.0%; Pred. No. 6,2e-73;
 Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 71 MCQVGRQALITGDDINRRYSEFQTMLOHLPATNAVEYFTKIATSLFESGINMGWVA 130
 DB 1 MCQVGRQALITGDDINRRYSEFQTMLOHLPATNAVEYFTKIATSLFESGINMGWVA 60
 QY 131 LIGFGYRLAHYOHGTLGQVTRFVVDMLHRCIARMTAORGGWVAALNLNGPIIN 190
 DB 61 LIGFGYRLAHYOHGTLGQVTRFVVDMLHRCIARMTAORGGWVAALNLNGPIIN 120
 QY 191 VLVLGVLLGQFVVRPFKS 211
 DB 121 VLVLGVLLGQFVVRPFKS 141
 RESULT 11
 AAW79535
 ID AAW79535 standard; Protein; 117 AA.
 XX
 AC AAW79535;
 XX
 DT 11-JAN-1999 (first entry)
 XX
 DE Truncated Bak polypeptide Bak-delta2-TM.
 XX
 KW Bak; bak binding protein; BBP; dbpbid-1; dbpbid-2; Bcl-2; apoptosis;
 KW cell death; cancer; lymphoma; neurodegeneration; heart disease;
 KW cell proliferation; infection; human; therapy; diagnosis.
 XX
 OS Homo sapiens.
 XX
 PN WO9841626-A1.
 XX
 PD 24-SEP-1998.
 XX
 PF 03-MAR-1998; 98WO-US04079.
 XX
 PR 09-JAN-1998; 98US-0071097.
 PR 20-MAR-1997; 97US-0041328.
 XX
 PA (LXRB-) LXR BIOTECHNOLOGY INC.
 XX
 PI Barr PJ, Fitzpatrick PA, Gibson HL, Kiefer MC;
 XX
 DR WPI; 1998-521220/44.
 XX
 PT New Bak-binding protein and related nucleic acid, vectors,
 PT transformed cells and antibodies - are useful for modulation of
 PT apoptosis in cancer, neuro-degeneration etc., also peptide fragments
 PT of Bak that interact with the protein
 XX
 PS Example 1; Page 53; 77pp; English.
 PS
 CC This is the amino acid sequence of Bak-delta2-TM, a truncated
 CC polypeptide comprising amino acids 71-187 of Bak (see AAW79534).
 CC A nucleotide sequence encoding Bak-delta2-TM was obtained from
 CC cDNA by PCR and cloned as an in-frame fusion to the GAL4-DNA
 CC binding domain in vector PAS2-1. The construct was used in a
 CC two-hybrid screen of human heart cDNA for the identification of
 CC clones encoding Bak binding proteins. The invention relates to a
 CC novel Bak binding protein (BBP, see AAW79537), the gene encoding BBP
 CC (see AAW61499), methods for detecting substances that alter the
 CC specific binding between Bak and BBP, as well as diagnostic and
 CC therapeutic methods utilizing BBP.
 CC

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XX DR WPI; 1996-485986/48.
XX DR N-PSDB; AAT42139.
XX PT Screening for anti-viral agents - by detecting the ability of an
XX PT agent to disrupt the interaction of a Bak protein and a viral
XX PT protein
XX PS Disclosure; Fig 2; 24pp; English.
XX CC This Bak-2 protein sequence represents a bcl-1 homologue which
XX CC interacts with Epstein-Barr virus (EBV) early lytic cycle BHRF1
XX CC protein, and is capable of modulating apoptosis. The protein may
XX CC be used in complete or partial form, or as an epitope tag fusion
XX CC protein, in a new virucide drug screening method, which involves
XX CC combination of Bak-2 protein and a viral protein (e.g. EBV BHRF1),
XX CC exposure to a test compound, and monitoring for disruption of the
XX CC interaction, e.g. by co-precipitation, protein interactive trapping
XX CC or ELISA. Interaction of Bak-2 and viral proteins allows viral
XX CC replication or latency in the absence of apoptosis. Compounds which
XX CC inhibit the interaction may be used as virucide, antitumour or
XX CC diagnostic agents.
XX SQ Sequence 211 AA;

Query Match 97.5%; Score 1075; DB 17; Length 211;
Best Local Similarity 97.2%; Pred. No. 6,8e-110;
Matches 205; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 1 MASGGGPGPPROEGCEPALPSASEEOVAODTEEEVFYSYFVRHQEOEAEGVAAPADPEM 60
DB 1 MASGGGPGPPROEGCEPALPSASEEOVAODTEEEVFYSYFVRHQEOEAEGVAAPADPEM 60
OY 61 VTLPLQPSSTMGQVGRQALAIIGDDINRRYDSEFQTMLOHLOPTAENAYEFTKIATSLFE 120
DB 61 VTLPLQPSSTMGQVGRQALAIIGDDINRRYDSEFQTMLOHLOPTAENAYEFTKIATSLFE 120
OY 121 SGINMGRRVVALLEGYRLALHYVOHGLTGFGLGOVTRFEVVDMLHHCIAARIARIGRGWVA 180
DB 121 SGINMGRRVVALLEGYRLALHYVOHGLTGFGLGOVTRFEVVDMLHHCIAARIARIGRGWVA 180
OY 181 LNLGNGPILNLVNLGVVLLGQFVVRREFKS 211
DB 181 LNLGNGPILNLVNLGVVLLGQFVVRREFKS 211

RESULT 8
AAV05432
ID AAV05432 standard; peptide; 208 AA.
XX AC AAV05432;
XX DT 02-JUL-1999 (first entry)
XX DE Mouse BAK protein sequence.
XX KW Bcl domain; cell death agonist; bcl homology domain; BCL-2 family;
XX KW apoptosis promoter; cancer cell; virus infected cell; inflammation;
XX KW autoantibody producing cell; cancer; lymphoproliferative condition;
XX KW arthritis; autoimmune disease; therapy.
XX OS Mus sp.
XX PN WO9916787-A1.
XX PD 08-APR-1999.
XX PF 22-SEP-1998; 98MO-US19765.
XX PR 07-OCT-1997; 97US-0946039.
XX PR 26-SEP-1997; 97US-0060133.
XX PA (UNIW ) UNIV WASHINGTON.

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XX PI Kormeyer SJ;
XX DR WPI; 1999-255058/21.
XX PT Bcl homology domain 3 polypeptide
XX PS Disclosure; Fig 2b; 104pp; English.
XX CC This sequence represents the murine BAK protein.
XX CC The invention relates to a bcl homology domain 3 (BH3 domain),
XX CC derived from a proapoptotic member of the BCL-2 family. The
XX CC BH3 polypeptide can be used in a method for promoting apoptosis in a
XX CC target cell, especially where the cell is a cancer cell a virus infected
XX CC cell or an autoantibody producing cell. The BH3 polypeptide can be used
XX CC in therapeutic compositions for treating disease including cancer, other
XX CC lymphoproliferative conditions, arthritis, inflammation, and autoimmune
XX CC diseases, which may result from the down regulation of cell death
XX CC regulation.
XX SQ Sequence 208 AA;

Query Match 75.2%; Score 829.5; DB 20; Length 208;
Best Local Similarity 76.3%; Pred. No. 7.1e-83;
Matches 161; Conservative 20; Mismatches 27; Indels 3; Gaps 2;

OY 1 MASGGGPGPPROEGCEPALPSASEEOVAODTEEEVFYSYFVRHQEOEAEGVAAPADPEM 60
DB 1 MASGGGPGPPKVGCDSE--PSPSEQVAODTEEEVFYSYFVRHQEOEQTGS-REPAPDEM 57
OY 61 VTLPLQPSSTMGQVGRQALAIIGDDINRRYDSEFQTMLOHLOPTAENAYEFTKIATSLFE 120
DB 58 DNLPLEPNSILGQVGRQALAIIGDDINRRYDSEFQTMLOHLOPTAGNAYEFTKIATSLFK 117
OY 121 SGINMGRRVVALLEGYRLALHYVOHGLTGFGLGOVTRFEVVDMLHHCIAARIARIGRGWVA 180
DB 118 SGISMGRRVVALLEGYRLALHYVOHGLTGFGLGOVTCFLADILLHAYTARIARIGRGWVA 177
OY 181 LNLGNGPILNLVNLGVVLLGQFVVRREFKS 211
DB 178 LNLRRDPILITVNLGVVLLGQFVVRREFKS 208

RESULT 9
AAR77879
ID AAR77879 standard; Protein; 152 AA.
XX AC AAR77879;
XX DT 21-NOV-1995 (first entry)
XX DE Human Cdn-1(60-211).
XX KW Cdn-1; apoptosis modulator; adoptive immunotherapy; therapy; HIV;
XX KW autoimmune disease; reperfusion injury; hepatitis; osteoporosis;
XX KW shock; lymphoma; eczema.
XX OS Homo sapiens.
XX PN WO9515084-A.
XX PD 08-JUN-1995.
XX PF 30-NOV-1994; 94MO-US13930.
XX PR 07-OCT-1994; 94US-0320157.
XX PR 30-NOV-1993; 93US-0160067.
XX PA (LXRB-) LXR BIOTECHNOLOGY INC.
XX PI Barr PJ, Kiefer MC;
XX DR WPI; 1995-215106/28.

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XX 22-SEP-1998; 98WO-US19765.
PF 07-OCT-1997; 97US-0946039.
XX 26-SEP-1997; 97US-0060133.
PA (UNIV) UNIV WASHINGTON.
XX Kormeyer SJ;
XX WPI; 1999-255058/21.
DR Bcl homology domain 3 polypeptide
XX
PT
PS Bcl homology domain 3 polypeptide
XX
XX Disclosure; Fig 21b; 104pp; English.
XX
XX This sequence represents the human BAK protein.
CC The invention relates to a bcl homology domain 3 (BH3 domain),
CC derived from a proapoptotic member of the BCL-2 family. The
CC BH3 polypeptide can be used in a method for promoting apoptosis in a
CC target cell, especially where the cell is a cancer cell a virus infected
CC cell or an autotantibody producing cell. The BH3 polypeptide can be used
CC in therapeutic compositions for treating disease including cancer, other
CC lymphoproliferative conditions, arthritis, inflammation, and autoimmune
CC diseases, which may result from the down regulation of cell death
CC regulation.
XX
XX
SQ Sequence 211 AA;

Query Match 100.0%; Score 1103; DB 20; Length 211;
Best Local Similarity 100.0%; Pred. No. 5.6e-113;
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MASGGGPPRQCEGEPALPSASEEQVAODTEVEFRSYVFRHQOEAEAGVAAPADPEM 60
DB 1 MASGGGPPRQCEGEPALPSASEEQVAODTEVEFRSYVFRHQOEAEAGVAAPADPEM 60
OY 61 VTLPPLQPSSTMGQVGRQLAIGDDINRRYDSEFQTMLOHLPFAENAYEFTKIATSLFE 120
DB 61 VTLPPLQPSSTMGQVGRQLAIGDDINRRYDSEFQTMLOHLPFAENAYEFTKIATSLFE 120
OY 121 SGINMGRRVALLGFGYRLAHVYOHGLTGFLGQVTRFVVDPMHHCIAHWIAORGWVAA 180
DB 121 SGINMGRRVALLGFGYRLAHVYOHGLTGFLGQVTRFVVDPMHHCIAHWIAORGWVAA 180
OY 181 LNLGNGPILNLVVLGVLLGQFVVRFRFES 211
DB 181 LNLGNGPILNLVVLGVLLGQFVVRFRFES 211

RESULT 6
AAR7877
ID AAR7877 standard; Protein; 211 AA.
XX
XX AAR7877;
XX
XX 21-NOV-1995 (first entry)
XX
XX Human Cdn-2.
XX
XX Cdn-2; apoptosis modulator; adoptive immunotherapy; therapy; HIV;
KW autoimmune disease; reperfusion injury; hepatitis, osteoporosis;
KW shock; lymphoma; eczema.
XX
XX Homo sapiens.
XX
XX W09515084-A.
XX
XX 08-JUN-1995.
XX
XX 30-NOV-1994; 94WO-US13930.
XX
XX 07-OCT-1994; 94US-0320157.
XX
XX

PR 30-NOV-1993; 93US-0160067.
XX
XX (LXRB-) LXR BIOTECHNOLOGY INC.
XX
XX Barr PJ, Kiefer MC;
XX
XX WPI; 1995-215106/28.
DR N-PSDB; AA095493.
XX
XX New nucleic acid sequences encoding Cdn apoptosis modulators - and
PT related vectors, transformed cells, proteins and antibodies, useful
PT or diagnosis and treatment e.g. of HIV infection, reperfusion injury
PT etc.
XX
XX Disclosure; Fig. 5D-E; 66pp; English.
XX
XX Cdn-2 cDNA was isolated from a human placental genomic library
CC using a 950 bp fragment of cdn-1 cDNA. Expression of cdn-2
CC in mouse progenitor B-cell Fc5.12 cells decreased IL-3-induced
CC apoptosis. The Cdn-2 protein displayed 97% amino acid identity
CC with Cdn-1 (AAR7876).
XX
XX
SQ Sequence 211 AA;

Query Match 97.5%; Score 1075; DB 16; Length 211;
Best Local Similarity 97.2%; Pred. No. 6.8e-110;
Matches 205; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 1 MASGGGPPRQCEGEPALPSASEEQVAODTEVEFRSYVFRHQOEAEAGVAAPADPEM 60
DB 1 MASGGGPPRQCEGEPALPSASEEQVAODTEVEFRSYVFRHQOEAEAGVAAPADPEM 60
OY 61 VTLPPLQPSSTMGQVGRQLAIGDDINRRYDSEFQTMLOHLPFAENAYEFTKIATSLFE 120
DB 61 VTLPPLQPSSTMGQVGRQLAIGDDINRRYDSEFQTMLOHLPFAENAYEFTKIATSLFE 120
OY 121 SGINMGRRVALLGFGYRLAHVYOHGLTGFLGQVTRFVVDPMHHCIAHWIAORGWVAA 180
DB 121 SGINMGRRVALLGFGYRLAHVYOHGLTGFLGQVTRFVVDPMHHCIAHWIAORGWVAA 180
OY 181 LNLGNGPILNLVVLGVLLGQFVVRFRFES 211
DB 181 LNLGNGPILNLVVLGVLLGQFVVRFRFES 211

RESULT 7
AAM03669
ID AAM03669 standard; Protein; 211 AA.
XX
XX AAM03669;
XX
XX 22-FEB-1997 (first entry)
XX
XX Bak-2 protein.
XX
XX Human; Bak-2; apoptosis; latency; virus replication;
KW Epstein-Barr virus; BHRF1; fusion protein; epitope tag;
KW drug screening; co-precipitation; ELISA; immunoassay; antibody;
KW protein interactive trapping; virucide; antitumour; diagnostic.
XX
XX Homo sapiens.
XX
XX W09633416-A1.
XX
XX 24-OCT-1996.
XX
XX 19-APR-1996; 96WO-US05639.
XX
XX 20-APR-1995; 95US-0426529.
XX
XX (LXRB-) LXR BIOTECHNOLOGY INC.
XX
XX Barr PJ, Kiefer MC;
XX
XX

Disclosure; Flg 1; 24pp; English.

DR N-PSDB; AAT17

New isolated human Bcl-Y protein - used to develop prods. for

GenCore version 5.1.4.p5.4578
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OK protein - protein search, using sw model

Run on: March 27, 2003, 10:44:18 (Search time 73 Seconds
(Without alignments)
385.149 Million cell updates/sec

Title: US-09-633-200-7
Perfect score: 1103
Sequence: 1 MASGGGPPRQEGCEPALP.....LVVLGVLLGQFVRRFFKS 211

Scoring table:
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Gapop 10.0, Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1103	100.0	211	16	AA077876
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6	1075	97.5	211	16	AA077877
7	1075	97.5	211	17	AA03669
8	829.5	75.2	208	20	AA05432
9	791	71.7	152	16	AA077879
10	737	66.8	141	16	AA077880

11	625	56.7	117	19	AA079535	Truncated Bak poly
12	609	55.2	116	16	AA077881	Human Cdn-1(96-211
13	609	55.2	116	16	AA079536	Truncated Bak poly
14	284	25.7	52	22	AA035127	Mammalian Bak alph
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16	192	17.4	239	22	AA064038	Human Bcl-2 protei
17	191.5	17.4	232	17	AA010120	Apoptosis-blockin
18	191.5	17.4	232	17	AA094347	Human Bcl-2 mutat
19	191	17.3	239	17	AA002383	Human Bcl-2. Homo
20	191	17.3	239	23	AA005227	Human D3A. caspase
21	190	17.2	239	14	AA080987	Sequence of bcl-2-
22	190	17.2	239	14	AA042312	Bcl-2 oncogene pro
23	190	17.2	239	15	AA047344	Human oncogene bcl
24	190	17.2	239	16	AA070331	Human bcl-2 protei
25	190	17.2	239	16	AA071404	Human bcl-2 alpha
26	190	17.2	239	19	AA040217	Human bcl-2. Homo
27	190	17.2	239	20	AA087812	A human bcl-2 alph
28	190	17.2	239	20	AA069203	Amino acid sequenc
29	190	17.2	239	22	AA008573	Human Bcl-2 protei
30	190	17.2	239	22	AA064035	Human Bcl-2 protei
31	190	17.2	239	22	AA064037	Human bcl-2alpha.
32	190	17.2	239	22	AA074129	Human bcl-2 protei
33	190	17.2	239	22	AA048288	Human Bcl-2 protei
34	190	17.2	239	22	AA050537	Protein sequence.
35	190	17.2	239	23	AA05986	Human bcl-2 proto-o
36	190	17.2	272	19	AA021120	Human bcl-2 protei
37	189.5	17.2	205	16	AA070332	Human thymus BCL-2
38	189.5	17.2	205	16	AA068886	Human bcl-2 beta p
39	189.5	17.2	205	16	AA071405	Human anti-apoptot
40	189.5	17.2	205	18	AA031529	bcl-2 polypeptide.
41	189.5	17.2	205	20	AA06319	A human bcl-2 beta
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45	189.5	17.2	205	23	AA075987	Protein sequence.

ALIGNMENTS

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XX	21-NOV-1995 (first entry)
DT	
XX	
XX	Human Cdn-1.
DE	
XX	Cdn-1; apoptosis modulator; adoptive immunotherapy; therapy; HIV;
KW	autoimmune disease; reperfusion injury; hepatitis; osteoporosis;
KW	shock; lymphoma; eczema.
OS	
XX	Homo sapiens.
XX	
PN	W09515084-A.
XX	
PD	08-JUN-1995.
XX	
PF	30-NOV-1994; 94WO-US13930.
XX	
XX	07-OCT-1994; 94US-0320157.
PR	30-NOV-1993; 93US-0160067.
XX	
PA	(LXRB-) LXR BIOTECHNOLOGY INC.
XX	
PI	Barr PJ, Kiefer MC;
XX	
XX	WPI; 1995-215106/28.
DR	N-PSDB; AA095492.
XX	
PT	New nucleic acid sequences encoding Cdn apoptosis modulators - and

GenCore version 5.1.4.P5.4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 27, 2003, 10:51:15 ; Search time 27 Seconds

(Without alignments)
229.935 Million cell updates/sec

Title: US-09-633-200-7

Perfect score: 1103
Sequence: 1 MASGGPPPPROEGEPALP.....LVVLGVLLGQFVRRFRKS 211

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 segs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1103	100.0	211	1	US-08-471-058-7 Sequence 7, Appl1
2	1103	100.0	211	1	US-08-471-058-10 Sequence 10, Appl1
3	1103	100.0	211	2	US-08-944-530-2 Sequence 2, Appl1
4	1103	100.0	211	3	US-08-471-057-7 Sequence 7, Appl1
5	1103	100.0	211	3	US-08-471-057-10 Sequence 10, Appl1
6	1103	100.0	211	4	US-09-381-488-2 Sequence 2, Appl1
7	1098	99.5	211	1	US-08-321-071A-16 Sequence 16, Appl1
8	1088.5	98.7	210	3	US-08-471-057-22 Sequence 22, Appl1
9	1075	97.5	211	1	US-08-471-058-9 Sequence 9, Appl1
10	1075	97.5	211	1	US-08-471-058-11 Sequence 11, Appl1
11	1075	97.5	211	2	US-08-944-530-4 Sequence 4, Appl1
12	1075	97.5	211	3	US-08-471-057-9 Sequence 9, Appl1
13	1075	97.5	211	3	US-08-471-057-11 Sequence 11, Appl1
14	791	71.7	152	1	US-08-471-058-22 Sequence 22, Appl1
15	737	66.8	141	4	US-09-381-488-4 Sequence 4, Appl1
16	625	56.7	117	4	US-08-471-058-23 Sequence 23, Appl1
17	609	55.2	116	4	US-08-471-058-24 Sequence 24, Appl1
18	609	55.2	116	4	US-09-381-488-5 Sequence 5, Appl1
19	304	27.6	57	1	US-08-321-071A-15 Sequence 15, Appl1
20	285	25.8	54	1	US-08-321-071A-21 Sequence 21, Appl1
21	284	25.7	52	4	US-09-127-048-5 Sequence 5, Appl1
22	251	22.8	49	1	US-08-321-071A-25 Sequence 25, Appl1
23	191.5	17.4	232	2	US-08-408-095-18 Sequence 18, Appl1
24	191	17.3	239	1	US-08-405-702A-12 Sequence 12, Appl1
25	190	17.2	239	1	US-08-333-565-51 Sequence 51, Appl1
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27	190	17.2	239	1	US-08-607-269-20 Sequence 20, Appl1

28	190	17.2	239	1	US-08-471-058-12 Sequence 12, Appl1
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ALIGNMENTS

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RESULT 1
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; Sequence 7, Application US/08471058
; Patent No. 5770443
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; GENERAL INFORMATION:
; APPLICANT: Kleier, Michael C.
; TITLE OF INVENTION: NOVEL APOPTOSIS MODULATING
; TITLE OF INVENTION: NOVEL APOPTOSIS MODULATING
; TITLE OF INVENTION: PROTEINS, DNA ENCODING THE PROTEINS AND METHODS OF USE
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESSES:
; ADDRESS: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,058
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/320,157
; FILING DATE: 07-OCT-1994
; APPLICATION NUMBER: 08/160,067
; FILING DATE: 30-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Lehnhardt, Susan K
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 23647-20007.12
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-813-5600
; TELEFAX: 415-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 211 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
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; US-08-471-058-7
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RESULT 4

US-08-471-057-7
; Sequence 7, Application US/08471057
; Patent No. 6015687
; GENERAL INFORMATION:
; APPLICANT: KIEFER, MICHAEL C.
; APPLICANT: BARB, PHILIP J.
; TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
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; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/320,157
; FILING DATE: 07-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: LEHNHARDT, SUSAN K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 23647-20007.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 211 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-471-057-7

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RESULT 5

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; Patent No. 6015687
; GENERAL INFORMATION:
; APPLICANT: KIEFER, MICHAEL C.
; APPLICANT: BARB, PHILIP J.
; TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,057
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/320,157
; FILING DATE: 07-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: LEHNHARDT, SUSAN K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 23647-20007.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 211 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-471-057-10

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Best Local Similarity 100.0%; Pred. No. 6.2e-117;
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Db 1 MASGGGPPRQCEGPALPSASEQVAQDTEEVFRSYVFRHQOEDAEAGVAPADPEM 60
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Db 61 VTLPQPSTMGQVQRQALAIIGDDINRRYDSEFOTMLQHOPTAENAYEFTFIATSLFE 120
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Db 121 SGIMNGRVALLGFGYRLALHYOHGLTGLGVTRFVVDPMHHCIAARMIAORGWVAA 180
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Db 181 LNLGNGPILNLVVLVGLGVLLGQFVVRFRFES 211
RESULT 6
US-09-381-488-2
; Sequence 2, Application US/09381488
; Patent No. 6441135

Thu Mar 27 11:12:58 2003

us-09-633-200-7.rai

Page 4

GENERAL INFORMATION:
APPLICANT: Kiefer, Michael C.
Gibson, Helen L.
Fitzpatrick, Paul A.
Barr, Philip J.

TITLE OF INVENTION: A NOVEL RAK BINDING PROTEIN, DNA
ENCODING THE PROTEIN, AND METHODS OF USE THEREOF

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESSES:
ADDRESSEE: BROWN, THERESA A.
STREET: 1560 Broadway, Suite 1200
CITY: Denver
STATE: CO
COUNTRY: USA
ZIP: 80202

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US-09/381,488
FILING DATE: 11-Feb-2000
CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: BROWN, THERESA A.
REGISTRATION NUMBER: 32,547
REFERENCE/DOCKET NUMBER: 4147-15-PUS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 211 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 2:

IS-09-381-488-2

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Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      121 SGIMGRYVALLGFRYRLAHYVQHGTLGFELOQYRFVVDENMLHHCIAKRWIAQGGWVAA 180
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Db      181 INLGNPILNVLVYLGAVLLGQFVVRFRFFKS 211

RESULT 7
US-08-321-071A-16
Sequence 16, Application US/08321071A
Patent No. 5672686
GENERAL INFORMATION:
APPLICANT: CHITTENDEN, Thomas D.
TITLE OF INVENTION: APOPTOSIS RELATED PROTEIN Bcl-2, AND METHODS
TITLE OF INVENTION: OF USE THEREOF
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr
STREET: 1455 Pennsylvania Avenue, N.W.

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CITY: Washington
STATE: D.C.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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APPLICATION NUMBER: US/08/321,071A
FILING DATE: 11-OCT-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10103
FILING DATE: 09-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/287,427
FILING DATE: 09-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: WIXON, HENRY N.
REGISTRATION NUMBER: 32, 073
REFERENCE/DOCKET NUMBER: 104322.121CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-942-8400
TELEFAX: 202-942-8484
INFORMATION FOR SEQ. ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 211 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-321-071A-16
Query Match 99.5%; Score 1098; DB 1; Length 211;
Best Local Similarity 99.5%; Pred. No. 2,3e-116;
Matches 210; Conservative 1; Mismatches 0; Indels 0; Gaps 0

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: Patent No. 6015687
: GENERAL INFORMATION:
: APPLICANT: KIEFER, MICHAEL C.
: APPLICANT: BARR, PHILIP J.
: TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA
: TITLE OF INVENTION: ENCODING THE PROTEINS AND METHODS OF USE THEREOF
: NUMBER OF SEQUENCES: 22
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: MORRISON & FOERSTER
: STREET: 755 Page Mill Road
: CITY: Palo Alto
: STATE: California
: COUNTRY: USA
: ZIP: 94304-1018
: COMPUTER READABLE FORM:

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,057
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/320,157
FILING DATE: 07-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: LEHNHARDT, SUSAN K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-20007.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 210 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-471-057-22

Query Match 98.7%; Score 1088.5; DB 3; Length 210;
Best Local Similarity 99.5%; Pred. No. 2.7e-115;
Matches 210; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MASGQGPPEPCGEPALPSASEEQVADTEVFPSYFYFHQDOEAEAGVAAPADPEM 60
Db 1 MASGQGPPEPCGEPALPSASEEQVADTEVFPSYFYFHQDOEAEAGVAAPADPEM 60
QY 61 VTLPLOPSSTMGQVGRQLAIGDINRRYDSEFQTMLOHLOPTAENAYEYFKIATSLFE 120
Db 61 VTLPLOPSSTMGQVGRQLAIGDINRRYDSEFQTMLOHLOPTAENAYEYFKIATSLFE 120
QY 121 SGINMGVVALLGFGRALAHVYQHGILGTGLGVTRFVVDPMIHHCIARWIAORGWVAA 180
Db 121 SGINMGVVALLGFGRALAHVYQHGILGTGLGVTRFVVDPMIHHCIARWIAORGWVAA 179
QY 181 LNLGNPILNLVNLVGLGVLLGQFVVRPFKS 211
Db 181 LNLGNPILNLVNLVGLGVLLGQFVVRPFKS 210

RESULT 9
US-08-471-058-9
Sequence 9, Application US/08471058
Patent No. 5770443
GENERAL INFORMATION:
APPLICANT: Kiefer, Michael C.
TITLE OF INVENTION: NOVEL APOPTOSIS MODULATING
TITLE OF INVENTION: PROTEINS, DNA ENCODING THE PROTEINS AND METHODS OF USE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,058

FILING DATE: 06-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/320,157
FILING DATE: 07-OCT-1994
APPLICATION NUMBER: 08/160,067
FILING DATE: 30-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Lehnhardt, Susan K
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-20007.12
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-813-5600
TELEFAX: 415-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 211 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-471-058-9

Query Match 97.5%; Score 1075; DB 1; Length 211;
Best Local Similarity 97.2%; Pred. No. 9.1e-114;
Matches 205; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 MASGQGPPEPCGEPALPSASEEQVADTEVFPSYFYFHQDOEAEAGVAAPADPEM 60
Db 1 MASGQGPPEPCGEPALPSASEEQVADTEVFPSYFYFHQDOEAEAGVAAPADPEM 60
QY 61 VTLPLOPSSTMGQVGRQLAIGDINRRYDSEFQTMLOHLOPTAENAYEYFKIATSLFE 120
Db 61 VTLPLOPSSTMGQVGRQLAIGDINRRYDSEFQTMLOHLOPTAENAYEYFKIATSLFE 120
QY 121 SGINMGVVALLGFGRALAHVYQHGILGTGLGVTRFVVDPMIHHCIARWIAORGWVAA 180
Db 121 SGINMGVVALLGFGRALAHVYQHGILGTGLGVTRFVVDPMIHHCIARWIAORGWVAA 180
QY 181 LNLGNPILNLVNLVGLGVLLGQFVVRPFKS 211
Db 181 LNLGNPILNLVNLVGLGVLLGQFVVRPFKS 211

RESULT 10
US-08-471-058-11
Sequence 11, Application US/08471058
Patent No. 5770443
GENERAL INFORMATION:
APPLICANT: Kiefer, Michael C.
TITLE OF INVENTION: NOVEL APOPTOSIS MODULATING
TITLE OF INVENTION: PROTEINS, DNA ENCODING THE PROTEINS AND METHODS OF USE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,058
FILING DATE: 06-JUN-1995
CLASSIFICATION: 800

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/320,157
FILING DATE: 07-OCT-1994
APPLICATION NUMBER: 08/160,067
FILING DATE: 30-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Lehnhardt, Susan K
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-20007.12
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-813-5600
TELEFAX: 415-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 211 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-471-058-11

Query Match 97.5%; Score 1075; DB 1; Length 211;
Best Local Similarity 97.2%; Pred. No. 9,1e-114;
Matches 205; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 MASGGGPPRQECGEPALPSASEEOVAODTEVEFRSYVYTRHQOEQAEGVAAPADPEM 60
DB 1 MASGGGPPRQECGEPALPSASEEOVAODTEVEFRSYVYTRHQOEQAEGVAAPADPEM 60
QY 61 VTLPLOPSSSTMGOVGRQLATIGDDINRRYDSEFQTMLOHLOPTAENAYEFTKIATSLFE 120
DB 61 VTLPLOPSSSTMGOVGRQLATIGDDINRRYDSEFQTMLOHLOPTAENAYEFTKIATSLFE 120
QY 121 SGIMNGRVVALLGFGYRLAHVYQHLGTGLGQVTRFVVDPMHHCIARWIAQRGWVAA 180
DB 121 SGIMNGRVVALLGFGYRLAHVYQHLGTGLGQVTRFVVDPMHHCIARWIAQRGWVAA 180
QY 181 LNLGNGPLNLVYLVGLVLLGQFVVRREFKS 211
DB 181 LNLGNGPLNLVYLVGLVLLGQFVVRREFKS 211

RESULT 11

US-08-944-530-4
Sequence 4, Application US/08944530
Patent No. 5998131
GENERAL INFORMATION:
APPLICANT: BARR, PHILIP J.
APPLICANT: KIEFER, MICHAEL C.
TITLE OF INVENTION: METHODS OF SCREENING FOR THERAPEUTIC
TITLE OF INVENTION: AGENTS USING NOVEL APOPTOSIS-MODULATING PROTEINS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,530
FILING DATE: 07-OCT-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/426,529
FILING DATE: 20-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: LEHNHARDT, SUSAN K.

REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-20007.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 211 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-944-530-4

Query Match 97.5%; Score 1075; DB 2; Length 211;
Best Local Similarity 97.2%; Pred. No. 9,1e-114;
Matches 205; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 MASGGGPPRQECGEPALPSASEEOVAODTEVEFRSYVYTRHQOEQAEGVAAPADPEM 60
DB 1 MASGGGPPRQECGEPALPSASEEOVAODTEVEFRSYVYTRHQOEQAEGVAAPADPEM 60
QY 61 VTLPLOPSSSTMGOVGRQLATIGDDINRRYDSEFQTMLOHLOPTAENAYEFTKIATSLFE 120
DB 61 VTLPLOPSSSTMGOVGRQLATIGDDINRRYDSEFQTMLOHLOPTAENAYEFTKIATSLFE 120
QY 121 SGIMNGRVVALLGFGYRLAHVYQHLGTGLGQVTRFVVDPMHHCIARWIAQRGWVAA 180
DB 121 SGIMNGRVVALLGFGYRLAHVYQHLGTGLGQVTRFVVDPMHHCIARWIAQRGWVAA 180
QY 181 LNLGNGPLNLVYLVGLVLLGQFVVRREFKS 211
DB 181 LNLGNGPLNLVYLVGLVLLGQFVVRREFKS 211

RESULT 12

US-08-471-057-9
Sequence 9, Application US/08471057
Patent No. 6015687
GENERAL INFORMATION:
APPLICANT: KIEFER, MICHAEL C.
APPLICANT: BARR, PHILIP J.
TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA
TITLE OF INVENTION: ENCODING THE PROTEINS AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,057
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/320,157
FILING DATE: 07-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: LEHNHARDT, SUSAN K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-20007.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:
LENGTH: 211 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-471-057-9

Query Match 97.5%; Score 1075; DB 3; Length 211;
Best Local Similarity 97.2%; Pred. No. 9,1e-114;
Matches 205; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 MASGOGPPPPROECGEPALPSASEEQVADTEVEFRSYFYFHQOEBAEGVAAPADPEM 60
DB 1 MASGOGPPPPROECGEPALPSASEEQVADTEVEFRSYFYFHQOEBAEGVAAPADPEM 60
QY 61 VTLPLOPSSMTGQVGRQALITGDDINRRYDSEFTMLQHLQPTAENAYEFTKTATSLFE 120
DB 61 VTLPLOPSSMTGQVGRQALITGDDINRRYDSEFTMLQHLQPTAENAYEFTKTATSLFE 120
QY 121 SGINMGRRVALLGFGRALAHYQGLTGLGQVTRFVVDMLHNCIARWIAORGWVAA 180
DB 121 SGINMGRRVALLGFGRALAHYQGLTGLGQVTRFVVDMLHNCIARWIAORGWVAA 180
QY 181 LNLGNGPILNLVYLGVVLLGQFVVRREFKS 211
DB 181 LNLGNGPILNLVYLGVVLLGQFVVRREFKS 211

RESULT 13

US-08-471-057-11
Sequence 11, Application US/08471057
Patent No. 6015687
GENERAL INFORMATION:
APPLICANT: KIEFER, MICHAEL C.
TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA
NUMBER OF INVENTION: ENCODING THE PROTEINS AND METHODS OF USE THEREOF
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471.057
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/320,157
FILING DATE: 07-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: LEHNHARDT, SUSAN K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-20007.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 211 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-471-057-11

Query Match 97.5%; Score 1075; DB 3; Length 211;
Best Local Similarity 97.2%; Pred. No. 9,1e-114;
Matches 205; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 MASGOGPPPPROECGEPALPSASEEQVADTEVEFRSYFYFHQOEBAEGVAAPADPEM 60
DB 1 MASGOGPPPPROECGEPALPSASEEQVADTEVEFRSYFYFHQOEBAEGVAAPADPEM 60
QY 61 VTLPLOPSSMTGQVGRQALITGDDINRRYDSEFTMLQHLQPTAENAYEFTKTATSLFE 120
DB 61 VTLPLOPSSMTGQVGRQALITGDDINRRYDSEFTMLQHLQPTAENAYEFTKTATSLFE 120
QY 121 SGINMGRRVALLGFGRALAHYQGLTGLGQVTRFVVDMLHNCIARWIAORGWVAA 180
DB 121 SGINMGRRVALLGFGRALAHYQGLTGLGQVTRFVVDMLHNCIARWIAORGWVAA 180
QY 181 LNLGNGPILNLVYLGVVLLGQFVVRREFKS 211
DB 181 LNLGNGPILNLVYLGVVLLGQFVVRREFKS 211

RESULT 14

US-08-471-058-22
Sequence 22, Application US/08471058
Patent No. 5770443
GENERAL INFORMATION:
APPLICANT: Kiefer, Michael C.
TITLE OF INVENTION: NOVEL APOPTOSIS MODULATING
PROTEINS, DNA ENCODING THE PROTEINS AND METHODS OF USE
NUMBER OF INVENTION: THEREOF
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471.058
FILING DATE: 06-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/320,157
FILING DATE: 07-OCT-1994
APPLICATION NUMBER: 08/160,067
FILING DATE: 30-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Lehnhardt, Susan K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-20007.12
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-813-5600
TELEFAX: 415-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 152 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-471-058-22

Query Match 71.7%; Score 791; DB 1; Length 152;
Best Local Similarity 100.0%; Pred. No. 8,2e-82;
Matches 152; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	120	ESGINMGVVALLGFGYRLALHYQHGILGFGQVRFVVDMLHHCIRMTAIGSGWVA	179
QY	61	ESGINMGVVALLGFGYRLALHYQHGILGFGQVRFVVDMLHHCIRMTAIGSGWVA	120
Db	180	ALNLNGPILNLVVLGVLGQFVVRRFPKS	211
QY	121	ALNLNGPILNLVVLGVLGQFVVRRFPKS	152

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OM protein - protein search, using sw model

Run on: March 27, 2003, 10:53:34 ; Search time 34 Seconds
(without alignments)
364.432 Million cell updates/sec

Title: US-09-633-200-7

Perfect score: 1103

Sequence: 1 MASGGGPPRQCEGPALP.....LVYGVVLGGFVVRREFKS 211

Scoring table: BLOSUM62

Searched: 237916 seqs, 58723674 residues

Total number of hits satisfying chosen parameters: 237916

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published_Applications_AA:*

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Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	1088.5	98.7	210	9	US-10-101-482-22
4	1075	97.5	211	9	US-10-101-482-9
5	1075	97.5	211	9	US-10-101-482-11
6	236	21.4	45	9	US-09-971-980-39
7	130	17.2	239	1	US-08-726-211-5
8	190	17.2	239	9	US-10-101-482-12
9	189.5	17.2	205	1	US-08-726-211-7
10	189.5	17.2	205	10	US-09-952-278-4
11	180	16.3	233	10	US-10-101-482-14
12	180	16.3	233	10	US-09-734-846-2
13	180	16.3	233	10	US-09-952-278-6
14	176	16.0	193	10	US-09-925-674A-7
15	174	15.8	193	10	US-09-925-674A-9
16	169	15.3	155	9	US-10-158-769-1
17	167.5	15.2	190	10	US-09-952-278-2
18	164	14.9	365	9	US-09-809-391-696
19	161.5	14.6	88	9	US-10-101-482-21

20	161	14.6	235	9	US-10-208-155-2	Sequence 2, Appl1
21	158.5	14.4	185	10	US-09-864-761-40954	Sequence 40954, A
22	158	14.3	152	9	US-10-158-769-2	Sequence 2, Appl1
23	143.5	13.0	226	9	US-10-101-482-15	Sequence 15, Appl1
24	143	13.0	192	9	US-10-101-482-13	Sequence 13, Appl1
25	143	13.0	331	10	US-09-033-525-2	Sequence 2, Appl1
26	132	12.0	213	10	US-09-682-667-2	Sequence 2, Appl1
27	127.5	11.6	213	10	US-09-682-667-6	Sequence 6, Appl1
28	126	11.4	176	9	US-10-102-806-657	Sequence 657, App
29	116	10.5	172	9	US-10-101-482-16	Sequence 16, Appl1
30	112	10.2	134	10	US-09-912-359-6	Sequence 6, Appl1
31	109.5	9.9	135	9	US-10-092-750-242	Sequence 242, App
32	107.5	9.7	63	10	US-09-952-278-3	Sequence 3, Appl1
33	98	8.9	24	10	US-09-682-667-16	Sequence 16, Appl1
34	97	8.8	170	10	US-09-682-667-4	Sequence 4, Appl1
35	95	8.6	170	10	US-09-682-667-8	Sequence 8, Appl1
36	91	8.3	28	9	US-10-092-750-152	Sequence 152, App
37	90	8.2	16	10	US-09-953-342-22	Sequence 22, Appl1
38	87	7.9	187	9	US-10-101-482-17	Sequence 17, Appl1
39	86.5	7.8	454	10	US-09-815-242-4877	Sequence 4877, Ap
40	86.5	7.8	474	10	US-09-815-242-10773	Sequence 10773, A
41	86.5	7.8	665	10	US-09-942-447-2	Sequence 2, Appl1
42	86	7.8	212	10	US-09-925-300-1577	Sequence 1577, Ap
43	85	7.7	17	9	US-10-092-750-240	Sequence 240, App
44	85	7.7	18	9	US-10-092-750-2	Sequence 2, Appl1
45	85	7.7	18	9	US-10-092-750-41	Sequence 41, Appl1

ALIGNMENTS

RESULT 1
US-10-101-482-7
Sequence 7, Application US/10101482
Publication No. US2003000837A1
GENERAL INFORMATION:
APPLICANT: KIEFER, MICHAEL C.
BARRE, PHILIP J.
TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA
ENCODING THE PROTEINS AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
City: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/101,482
FILING DATE: 18-Mar-2002
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/320,157
FILING DATE: 07-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: LEHNHARDT, SUSAN K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-20007.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 211 amino acids
TYPE: amino acid
TOPOLOGY: linear

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; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-101-482-7

Query Match
Best Local Similarity 100.0%; Score 1103; DB 9; Length 211;
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASGCGPPPPROECGEPALPSASEQVADTEEVFRSYVFRHQOEAGVAAADPEM 60
DB 1 MASGCGPPPPROECGEPALPSASEQVADTEEVFRSYVFRHQOEAGVAAADPEM 60
QY 61 VTLPDPSTMGVGRQLAIGDDINRRYDSEFOTMLQHPAENAYEFTKATSLFE 120
DB 61 VTLPDPSTMGVGRQLAIGDDINRRYDSEFOTMLQHPAENAYEFTKATSLFE 120
QY 121 SGIMNGRVALLGFGYRLAHVYOHGLTGLGQVTRFVDFMLHHCIAFWIAORGWVAA 180
DB 121 SGIMNGRVALLGFGYRLAHVYOHGLTGLGQVTRFVDFMLHHCIAFWIAORGWVAA 180
QY 181 LNLGNGPLNLVVLVGLVLLGQFVVRREFKS 211
DB 181 LNLGNGPLNLVVLVGLVLLGQFVVRREFKS 211

RESULT 2
US-10-101-482-10
; Sequence 10, Application US/10101482
; Publication No. US2003000837A1
; GENERAL INFORMATION:
; APPLICANT: KIEFER, MICHAEL C.
; BARR, PHILIP J.
; TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA
; ENCODING THE PROTEINS AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESS: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/101,482
; FILING DATE: 18-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/320,157
; FILING DATE: 07-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: LEHNHARDT, SUSAN K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 23647-20007.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 211 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-101-482-10

Query Match
Best Local Similarity 100.0%; Score 1103; DB 9; Length 211;
Matches 211; Conservative 100.0%; Pred. No. 1.5e-105;
```

```
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASGCGPPPPROECGEPALPSASEQVADTEEVFRSYVFRHQOEAGVAAADPEM 60
DB 1 MASGCGPPPPROECGEPALPSASEQVADTEEVFRSYVFRHQOEAGVAAADPEM 60
QY 61 VTLPDPSTMGVGRQLAIGDDINRRYDSEFOTMLQHPAENAYEFTKATSLFE 120
DB 61 VTLPDPSTMGVGRQLAIGDDINRRYDSEFOTMLQHPAENAYEFTKATSLFE 120
QY 121 SGIMNGRVALLGFGYRLAHVYOHGLTGLGQVTRFVDFMLHHCIAFWIAORGWVAA 180
DB 121 SGIMNGRVALLGFGYRLAHVYOHGLTGLGQVTRFVDFMLHHCIAFWIAORGWVAA 180
QY 181 LNLGNGPLNLVVLVGLVLLGQFVVRREFKS 211
DB 181 LNLGNGPLNLVVLVGLVLLGQFVVRREFKS 211

RESULT 3
US-10-101-482-22
; Sequence 22, Application US/10101482
; Publication No. US2003000837A1
; GENERAL INFORMATION:
; APPLICANT: KIEFER, MICHAEL C.
; BARR, PHILIP J.
; TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA
; ENCODING THE PROTEINS AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESS: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/101,482
; FILING DATE: 18-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/320,157
; FILING DATE: 07-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: LEHNHARDT, SUSAN K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 23647-20007.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 210 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-10-101-482-22

Query Match
Best Local Similarity 98.7%; Score 1088.5; DB 9; Length 210;
Matches 210; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MASGCGPPPPROECGEPALPSASEQVADTEEVFRSYVFRHQOEAGVAAADPEM 60
DB 1 MASGCGPPPPROECGEPALPSASEQVADTEEVFRSYVFRHQOEAGVAAADPEM 60
```

QY 61 VTLPDPSSTMGVGRQLAIIIGDDINRRYDSEFQTMLOHLOPTAENAYEFTKIATSLFE 120
 Db 61 VTLPDPSSTMGVGRQLAIIIGDDINRRYDSEFQTMLOHLOPTAENAYEFTKIATSLFE 120
 QY 121 SGINMGRRVVALGFGYRLALHYOHGLTGLGQVTRFVDFMLHHCIARWIAORGWVAA 180
 Db 121 SGINMGRRVVALGFGYRLALHYOHGLTGLGQVTRFVDFMLHHCIARWIAORGWVAA 179
 QY 181 LNLGNPILNLVNLVGLVLLGQFVVRREFKS 211
 Db 180 LNLGNPILNLVNLVGLVLLGQFVVRREFKS 210

RESULT 4
 US-10-101-482-9

; Sequence 9, Application US/10101482
 ; Publication No. US2003000837A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KIEFER, MICHAEL C.
 ; BARR, PHILIP J.
 ; TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA
 ; ENCODING THE PROTEINS AND METHODS OF USE THEREOF
 ; NUMBER OF SEQUENCES: 22
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MORRISON & FOERSTER
 ; STREET: 755 Page Mill Road
 ; CITY: Palo Alto
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94304-1018
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/101,482
 ; FILING DATE: 18-Mar-2002
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/320,157
 ; FILING DATE: 07-OCT-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: LEHNHARDT, SUSAN K.
 ; REGISTRATION NUMBER: 33,943
 ; REFERENCE/DOCKET NUMBER: 23647-20007, 20
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 813-5600
 ; TELEFAX: (415) 494-0792
 ; TELEX: 706141
 ; INFORMATION FOR SEQ ID NO: 9:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 211 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
 US-10-101-482-9

Query Match 97.5%; Score 1075; DB 9; Length 211;
 Best Local Similarity 97.2%; Pred. No. 1.1e-102;
 Matches 205; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 MASGGGPPRRQEGCEPALPSASEQVAODTEEFYRSYVYRHOQOEAGVAAPADPEM 60
 Db 1 MASGGGPPRRQEGCEPALPSASEQVAODTEEFYRSYVYRHOQOEAGVAAPADPEM 60
 QY 61 VTLPDPSSTMGVGRQLAIIIGDDINRRYDSEFQTMLOHLOPTAENAYEFTKIATSLFE 120
 Db 61 VTLPDPSSTMGVGRQLAIIIGDDINRRYDSEFQTMLOHLOPTAENAYEFTKIATSLFE 120
 QY 121 SGINMGRRVVALGFGYRLALHYOHGLTGLGQVTRFVDFMLHHCIARWIAORGWVAA 180
 Db 121 SGINMGRRVVALGFGYRLALHYOHGLTGLGQVTRFVDFMLHHCIARWIAORGWVAA 180

Db 121 SGINMGRRVVALGFGYRLALHYOHGLTGLGQVTRFVDFMLHHCIARWIAORGWVAA 180
 QY 181 LNLGNPILNLVNLVGLVLLGQFVVRREFKS 211
 Db 181 LNLGNPILNLVNLVGLVLLGQFVVRREFKS 211

RESULT 5
 US-10-101-482-11

; Sequence 11, Application US/10101482
 ; Publication No. US2003000837A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KIEFER, MICHAEL C.
 ; BARR, PHILIP J.
 ; TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA
 ; ENCODING THE PROTEINS AND METHODS OF USE THEREOF
 ; NUMBER OF SEQUENCES: 22
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MORRISON & FOERSTER
 ; STREET: 755 Page Mill Road
 ; CITY: Palo Alto
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94304-1018
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/101,482
 ; FILING DATE: 18-Mar-2002
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/320,157
 ; FILING DATE: 07-OCT-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: LEHNHARDT, SUSAN K.
 ; REGISTRATION NUMBER: 33,943
 ; REFERENCE/DOCKET NUMBER: 23647-20007, 20
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 813-5600
 ; TELEFAX: (415) 494-0792
 ; TELEX: 706141
 ; INFORMATION FOR SEQ ID NO: 11:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 211 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
 US-10-101-482-11

Query Match 97.5%; Score 1075; DB 9; Length 211;
 Best Local Similarity 97.2%; Pred. No. 1.1e-102;
 Matches 205; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 MASGGGPPRRQEGCEPALPSASEQVAODTEEFYRSYVYRHOQOEAGVAAPADPEM 60
 Db 1 MASGGGPPRRQEGCEPALPSASEQVAODTEEFYRSYVYRHOQOEAGVAAPADPEM 60
 QY 61 VTLPDPSSTMGVGRQLAIIIGDDINRRYDSEFQTMLOHLOPTAENAYEFTKIATSLFE 120
 Db 61 VTLPDPSSTMGVGRQLAIIIGDDINRRYDSEFQTMLOHLOPTAENAYEFTKIATSLFE 120
 QY 121 SGINMGRRVVALGFGYRLALHYOHGLTGLGQVTRFVDFMLHHCIARWIAORGWVAA 180
 Db 121 SGINMGRRVVALGFGYRLALHYOHGLTGLGQVTRFVDFMLHHCIARWIAORGWVAA 180
 QY 181 LNLGNPILNLVNLVGLVLLGQFVVRREFKS 211
 Db 181 LNLGNPILNLVNLVGLVLLGQFVVRREFKS 211

RESULT 6
US-09-971-980-39
Sequence 39, Application US/09971980
Patent No. US2002016439A1
GENERAL INFORMATION:
APPLICANT: Weiner, David B.
APPLICANT: Yang, Joo-Sung
TITLE OF INVENTION: Compositions and Methods of Using Capsid Protein From Flavivirus
FILE REFERENCE: Upn-4105
CURRENT APPLICATION NUMBER: US/09/971,980
CURRENT FILING DATE: 2001-10-04
PRIOR APPLICATION NUMBER: 60/237,885
PRIOR FILING DATE: 2000-10-04
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 39
LENGTH: 45
TYPE: PRF
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: No. US2002016439A1el Sequence
US-09-971-980-39

Query Match 21.4%; Score 236; DB 9; Length 45;
Best Local Similarity 100.0%; Pred. No. 1.8e-17;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 163 LHHCIARWIAORGWVAALNLGNGPILNVLVGVLLGQFVRR 207
DB 1 LHHCIARWIAORGWVAALNLGNGPILNVLVGVLLGQFVRR 45

RESULT 7
US-08-726-211-5
Sequence 5, Application US/08726211
Publication No. US20030012812A1
GENERAL INFORMATION:
APPLICANT: Torino, Mar
APPLICANT: Tati, Ana M.
APPLICANT: Lopez-Berestein, Gabriel
TITLE OF INVENTION: INHIBITION OF Bcl-2 PROTEIN EXPRESSION BY
TITLE OF INVENTION: LIPOSOMAL ANTISENSE OLIGODEOXYNUCLEOTIDES
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: United States of America
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/726,211
FILING DATE: Concurrently Herewith
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mark B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: UTXC:504
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 239 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-726-211-5
Query Match 17.2%; Score 190; DB 1; Length 239;
Best Local Similarity 26.4%; Pred. No. 9.6e-12;
Matches 58; Conservative 31; Mismatches 81; Indels 50; Gaps 8;
QY 30 DDEEVRSEYVYFRHQQ---EQEAGV-----AAPA-----DPEMYT 62
DB 10 DREELVMKRIYHKLSQREMDADGAGAPGAPGIRFSQPGHTPHPAASRDVART 69
QY 63 IPLQ-PSSTMGVGRQIAIT-----GDDINRYSEFGTLMQHLQPTAENAYEY 110
DB 70 SPLQTPAAPAGAAAGPALSPPVYVHLARQAGDPSRRYKDEKMSQLHLTPFARGR 129
QY 111 FKIKATSLFEESINMGRRVALFGYRLALHYOHGLTGFQGYTRPVDFMLHICIAW 170
DB 130 FATVVEELFRDGVNMGRIYAFEFEGVWCYSVARESPVDNALMWTLYLRH-LHTW 188
QY 171 IAORGWVAALNLGNGPIT-----LNLVLGVLLG 201
DB 189 IDNGGMDAFVEL-YGPSWRPLDFSWLTKLTLLALVG 227

RESULT 8
US-10-101-482-12
Sequence 12, Application US/10101482
Publication No. US20030008837A1
GENERAL INFORMATION:
APPLICANT: KIEFER, MICHAEL C.
APPLICANT: BARR, PHILIP J.
TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA
ENCODING THE PROTEINS AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESSES:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/101,482
FILING DATE: 18-Mar-2002
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/320,157
FILING DATE: 07-Oct-1994
ATTORNEY/AGENT INFORMATION:
NAME: LEHNHARDT, SUSAN K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-20007.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 239 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-101-482-12
Query Match 17.2%; Score 190; DB 9; Length 239;
Best Local Similarity 26.4%; Pred. No. 9.6e-12;
Matches 58; Conservative 32; Mismatches 80; Indels 50; Gaps 8;

```

QY 30 DTEEVRSYVYRRHQ---EQAEQV-----AAPA-----DPEAVT 62
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 10 DNREIVMKYIHKLSQRYGEMDADGVAAPGAPAPGIFSSQPGHTPHTPAASRDPAVT 69
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 63 LPLQ-PSSTMGQVGRQLAIT-----GDDINRRYDSEFQTMLOHLOPTAENAYEY 110
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 70 SPLQTPAAPGAAGAPALSPVPVYVHLALRQAGDDFSRRYRDRDFAEMSRQLHLTPFTAGR 129
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 111 FTKIATSLFESGIMGVAVALLGFGYRLALHYVQHGLTGLGQYTRPVYDMLHHCIARW 170
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 130 FATVEELFRDGVNMGRIYVAFEEFGVWCYVSVRNREMSPLVDNIALMTEYLNRRH-LHTW 188
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 171 IAORGWVAALNLG 184
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 189 IQDNGGWGASGDVSLG 205
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT 9

```

US-08-726-211-7
; Sequence 7, Application US/08726211
; Publication No. US20030012812A1
; GENERAL INFORMATION:
; APPLICANT: Tormo, Mar
; APPLICANT: Tati, Ana M.
; APPLICANT: Lopez-Berestein, Gabriel
; TITLE OF INVENTION: INHIBITION OF Bcl-2 PROTEIN EXPRESSION BY
; TITLE OF INVENTION: LIPOSOMAL ANTISENSE OLIGODEOXYNUCLEOTIDES
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/726/211
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: UTXC:504
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 205 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-726-211-7

```

Query Match 17.2%; Score 189.5; DB 1; Length 205;
 Best Local Similarity 27.4%; Pred. No. 8.7e-12;
 Matches 54; Conservative 27; Mismatches 73; Indels 43; Gaps 7;

```

QY 30 DTEEVRSYVYRRHQ---EQAEQV-----AAPA-----DPEAVT 62
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 10 DNREIVMKYIHKLSQRYGEMDADGVAAPGAPAPGIFSSQPGHTPHTPAASRDPAVT 69
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 63 LPLQ-PSSTMGQVGRQLAIT-----GDDINRRYDSEFQTMLOHLOPTAENAYEY 110
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 70 SPLQTPAAPGAAGAPALSPVPVYVHLALRQAGDDFSRRYRDRDFAEMSRQLHLTPFTAGR 129
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 111 FTKIATSLFESGIMGVAVALLGFGYRLALHYVQHGLTGLGQYTRPVYDMLHHCIARW 170
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```

Db 130 FATVEELFRDGVNMGRIYVAFEEFGVWCYVSVRNREMSPLVDNIALMTEYLNRRH-LHTW 188
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 171 IAORGWVAALNLG 184
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 189 IQDNGGWGASGDVSLG 205
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT 10

```

US-09-952-278-4
; Sequence 4, Application US/09952278
; Patent No. US20020137182A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Craig B.
; APPLICANT: Boise, Lawrence H.
; TITLE OF INVENTION: Vertebrate Apoptosis Gene:
; COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: 321 No. US20020137182A1th Clark Street, Suite 800
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60610
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/952/278
; FILING DATE: 12-Sep-2001
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/081/448
; FILING DATE: <unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: No. US20020137182A1thrup, Thomas E.
; REGISTRATION NUMBER: 33,268
; REFERENCE/DOCKET NUMBER: ARCD090
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-744-0090
; TELEFAX: 312-755-4489
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 205 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-952-278-4

```

Query Match 17.2%; Score 189.5; DB 10; Length 205;
 Best Local Similarity 27.4%; Pred. No. 8.7e-12;
 Matches 54; Conservative 27; Mismatches 73; Indels 43; Gaps 7;

```

QY 30 DTEEVRSYVYRRHQ---EQAEQV-----AAPA-----DPEAVT 62
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 10 DNREIVMKYIHKLSQRYGEMDADGVAAPGAPAPGIFSSQPGHTPHTPAASRDPAVT 69
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 63 LPLQ-PSSTMGQVGRQLAIT-----GDDINRRYDSEFQTMLOHLOPTAENAYEY 110
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 70 SPLQTPAAPGAAGAPALSPVPVYVHLALRQAGDDFSRRYRDRDFAEMSRQLHLTPFTAGR 129
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 111 FTKIATSLFESGIMGVAVALLGFGYRLALHYVQHGLTGLGQYTRPVYDMLHHCIARW 170
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 130 FATVEELFRDGVNMGRIYVAFEEFGVWCYVSVRNREMSPLVDNIALMTEYLNRRH-LHTW 188
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 171 IAORGWVAALNLG 184
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 189 IQDNGGWGASGDVSLG 205
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```

1  APPLICANT: Nickoloff, Brian J.
2  APPLICANT: Zhang, Qingqiang
3  TITLE OR INVENTION: Antisense Modulation of bcl-x Expression
4  FILE REFERENCE: ISPh-0528
5  CURRENT APPLICATION NUMBER: US/09/734,846
6  PRIOR APPLICATION NUMBER: 2000-12-12
7  PRIOR FILING DATE: 09/277,020
8  PRIOR APPLICATION NUMBER: 1998-03-26
9  PRIOR FILING DATE: 09/167,921
10 PRIOR APPLICATION NUMBER: 1998-10-07
11 PRIOR FILING DATE: 09/323,743
12 PRIOR APPLICATION NUMBER: 1999-06-02
13 PRIOR FILING DATE: 1999-06-02
14 NUMBER OF SEQ ID NOS: 74
15 SOFTWARE: PatentIn Ver. 2.0
16 SEQ ID NO 2
17 LENGTH: 233
18 TYPE: PRT
19 ORGANISM: Homo sapiens
20 US-09-734-846-2

```

```

Query Match Similarity      16.3% Score 180; DB 10; Length 233;
Best Local Similarity      28.3%; Pred. No. 9.8e-11;
Matches    43; Conservative   22; Mismatches   71; Indels   16; Gaps   3.

OY       71 MGQVROLATLIDDDINRRYSDFQTMLDLPDTAENAYEFTFKIATSLESGINNGRVYA 130
           | : | : ||| : | : | : | : | : | : | : | : | : | : | : | : | :
DB        83 MAAYGALREADDEDELRYRRAFSDLTSLHTTPGTAYOSFEQVYNLEFRDSGVNNGRIYA 142

OY       131 LIGFGRLALHYQGILGFGLGOYRVFYVDPLHCHIAWIMARGGWAAALNL-GNGP-- 187
           | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
DB        143 PFSFGLACVESVDKEMQVLVSRIAAMMYTYLNDR-LFWPIQDNCGMDTFVELLYGNAAA 201

OY       188 -----LLNVLVYLGVLLGGQEVVR 207
           | : | ||||| : | :
DB        202 ESRKGGERNRWFELTGMTYAGVVLLGSLSRK 233

RESULT 13
US-09-952-278-6
Sequence 6, Application US-/09952278
Patent No. US20020137182A1
GENERAL INFORMATION:
APPLICANT: Thompson, Craig B.
             Boise, Lawrence H.
TITLE OF INVENTION: Vertebrate Apoptosis Gene:
                   Compositions and Methods
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: 321 No. US20020137182Alch Clark Street, Suite 800
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60610
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/952,278
FILING DATE: 12-Sep-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/081,448
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: NO. US20020137182Althrup, Thomas E.
REGISTRATION NUMBER: 33,268
REFERENCE/DOCKET NUMBER: ARCD090
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-744-0090
TELEFAX: 312-755-4489
```

```

; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 233 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
;   SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-952-278-6

```

```

Query Match      16.3%; Score 180; DB 10; Length 233;
Best Local Similarity 28.3%; Pred. No. 9.8e-11;
Matches 43; Conservative 22; Mismatches 71; Indels 16; Gaps 3;

```

```

QY 71 MGQVQQLAIIIDDDINRRYDSEFQTMLOPTAENAYEFYFKTATSLFESGIMNGRYVA 130
DB 83 MAAYKQALEADDEFELRYRAFSDLTSQHLITPGTAQSEQYVNNELFRDGVNMGRIVA 142
QY 131 LIGFGYRLAHYQHGLTGFQGYTRFVYDMLHHCIAKRWIAQRGVAALNL-GNGP-- 187
DB 143 FFSFGALCVESVDKEMQYLVSRIAAMWATYLNDR-LEPWIOENGWDTFVELYGNNA 201
QY 188 -----LNVVLVGLVLLGQFVRR 207
DB 202 ESRKQGERFNRWFLTGMVTAGVYLLGLFSRK 233

```

```

RESULT 14
US-09-925-674A-7
; Sequence 7, Application US/09925674A
; Patent No. US20020119943A1
; GENERAL INFORMATION:
; APPLICANT: AMRAD Operations Pty Ltd
; TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-w, BELONGS TO THE bcl-2
; FILE REFERENCE: 11686a
; CURRENT APPLICATION NUMBER: US/09/925,674A
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 09/925,674
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: PN8965
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 7
; LENGTH: 193
; TYPE: PRT
; ORGANISM: HUMAN
US-09-925-674A-7

```

```

Query Match      16.0%; Score 176; DB 10; Length 193;
Best Local Similarity 28.2%; Pred. No. 1.9e-10;
Matches 57; Conservative 25; Mismatches 86; Indels 34; Gaps 6;

```

```

QY 28 AADTEVPSRYVYRHQOE-----QAEQVAAPADDEMYTLPLQPSSTMGOVROLAIIIGD 83
DB 7  APTDRLVADPFGYKLRQGYVCGAGPGEGPADP-----LHQAMRAAGD 51
QY 84 DINRRYDSEFQTMLOPTAENAYEFYFKTATSLFESGIMNGRYVALLGQYRLAHYQH 143
DB 52 EETFRRTFSDLAQHLHTPGSAQORTQVSDLEFGGPMNGRLVAFVFGAALCAESV 111
QY 144 QHGLTGFQGYTRFVYDMLHHCIAKRWIAQRGVA-----AALNIGNGPILNV 191
DB 112 NKEMEPYGVQVEMWVAY-LETRLADWIIHSSGMAEFYALYGDGALAEARLRREGNMA 170
QY 192 LVVL-GVLLGQFV-VRRFEKS 211
DB 171 RFLVLTGAVALLGALTYVGAFFAS 192

```

```

RESULT 15
US-09-925-674A-9
; Sequence 9, Application US/09925674A

```

```

; Patent No. US20020119943A1
; GENERAL INFORMATION:
; APPLICANT: AMRAD Operations Pty Ltd
; TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-w, BELONGS TO THE bcl-2
; FILE REFERENCE: 11686a
; CURRENT APPLICATION NUMBER: US/09/925,674A
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 09/925,674
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: PN8965
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 9
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Mouse
US-09-925-674A-9

```

```

Query Match      15.8%; Score 174; DB 10; Length 193;
Best Local Similarity 28.5%; Pred. No. 3.1e-10;
Matches 57; Conservative 24; Mismatches 85; Indels 34; Gaps 6;

```

```

QY 30 DTEEVFRSYVYRHQOE-----QAEQVAAPADDEMYTLPLQPSSTMGOVROLAIIIGD 85
DB 9  DTRALVADPFGYKLRQGYVCGAGPGEGPADP-----LHQAMRAAGDEF 53
QY 86 NRRYDSEFQTMLOPTAENAYEFYFKTATSLFESGIMNGRYVALLGQYRLAHYQH 145
DB 54 ETRRRRTFSDLAQHLHTPGSAQORTQVSDLEFGGPMNGRLVAFVFGAALCAESV 113
QY 146 GLTGFQGYTRFVYDMLHHCIAKRWIAQRGVA-----AALNIGNGPILNV 193
DB 114 EMEPLVQVQVDMWVAY-LETRLADWIIHSSGMAEFYALYGDGALAEARLRREGNMA 172
QY 194 VL-GVLLGQFV-VRRFEKS 211
DB 173 VLTGAVALLGALTYVGAFFAS 192

```

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Search completed: March 27, 2003, 10:58:55
Job time : 34 secs

```


GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: March 27, 2003, 10:50:54 / Search time 21 seconds
(without alignments)
965.922 Million cell updates/sec

Title: US-09-633-200-7

Perfect score: 1103
Sequence: 1 MASGGGPGPPROCEGPALP.....LVVLGVLLGPFVVRFRFS 211

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR73:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1103	100.0	211	2	S58873
2	1075	97.5	211	2	S58875
3	189.5	17.2	205	1	TVHUB1
4	189	17.1	239	1	TVHUB1
5	183.5	16.6	233	2	A37332
6	181	16.4	233	2	I49056
7	181	16.4	233	2	S51761
8	180	16.3	233	2	B47537
9	178.5	16.2	199	1	TVMSB1
10	177	16.0	236	1	TVMSA1
11	176.5	16.0	236	1	I53744
12	174.5	15.8	216	2	B37332
13	173.5	15.7	233	2	I67431
14	172.5	15.6	236	2	JC7383
15	170.5	15.5	236	2	I67432
16	167.5	15.2	190	2	A47537
17	164	14.9	227	2	JEO203
18	160.5	14.6	232	2	S24390
19	158.5	14.4	214	2	I49057
20	146	13.2	218	2	B47538
21	143.5	13.0	350	2	A47476
22	143	13.0	192	2	A47538
23	143	13.0	192	2	D47538
24	142	12.9	179	2	JC7255
25	126	11.4	133	2	I53295
26	122	11.1	154	2	I58194
27	116	10.5	172	2	I49449
28	112	10.2	175	2	I39055
29	109	9.9	143	2	I38921

30	107.5	9.7	177	2	S54778
31	90.5	8.2	373	2	B75542
32	88	8.0	255	2	JC7567
33	86.5	7.8	876	2	AB1177
34	86.5	7.8	876	2	AP1534
35	86	7.8	345	2	T08563
36	85.5	7.8	1237	2	A56764
37	81.5	7.4	416	2	E97579
38	81.5	7.4	742	2	T00371
39	81	7.3	1021	2	AC2202
40	80.5	7.3	272	2	C75560
41	80.5	7.3	420	2	DB3952
42	80.5	7.3	2406	2	A54148
43	80.5	7.3	2515	2	S47008
44	80	7.3	133	1	GPBP4
45	80	7.3	865	2	A25104

ALIGNMENTS

RESULT 1

S58873

Bak protein - human

N:Alternate names: bcl-2 homolog; cdc-1 protein

C:Species: Homo sapiens (man)

C:Date: 15-Feb-1996 #sequence-revision 01-Mar-1996 #text-change 08-Oct-1999

C:Accession: S58873; S58872; S58874

R:Chittenden, T.; Harrington, E.A.; O'Connor, R.; Flemington, C.; Lutz, R.J.; Evan, G.

Nature 374, 733-736, 1995

A:Title: Induction of apoptosis by the Bcl-2 homologous Bak.

A:Reference number: S58873; MUID:95231653; PMID:7715730

A:Accession: S58873

A>Status: preliminary; nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-211 <CHI>

A:Cross-references: EMBL:U23765; NID:q758797; PIDN:AAA93066.1; PID:q758798

R:Farrow, S.N.; White, J.H.M.; Martinou, I.; Raven, T.; Pun, K.T.; Grindham, C.J.; Mar

Nature 374, 736-739, 1995

A:Title: Modulation of apoptosis by the widely distributed Bcl-2 homologous Bak.

A:Reference number: S58874; MUID:95231654; PMID:7715731

A:Accession: S58874

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-211 <KIE>

A:Cross-references: EMBL:U16811; NID:q595923; PIDN:AAA74466.1; PID:q595924

C:Genetics:

A:Gene: GDB:BAK

A:Cross-references: GDB:635887

Query Match

Best Local Similarity 100.0%; Score 1103; DB 2; Length 211;

Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MASGGGPGPPROCEGPALPSASEEOVAODTEVFYSYFRRHQCEAEAGVAAPADPEM	60
DB	1	MASGGGPGPPROCEGPALPSASEEOVAODTEVFYSYFRRHQCEAEAGVAAPADPEM	60
QY	61	VTPLPDPSSTMGVQGLAIGDINRRYDSEFOTMLQHLQTAENAVYEFKTIATSLPE	120
DB	61	VTPLPDPSSTMGVQGLAIGDINRRYDSEFOTMLQHLQTAENAVYEFKTIATSLPE	120
QY	121	SGINMGVAVALLGFGYRLALHYVQHGLTGFLGVYDFYVDMLHICIAWNIORSGWVA	180

Db 121 SGINMGKRVALLGGRRLALHYQHGLTGFLGQVTRFVYDMLHHCIAIRWIAQRGWAA 180
 Oy 181 LNLGNGPILNLVVLGVLLGQFVVRREFKS 211
 Db 181 LNLGNGPILNLVVLGVLLGQFVVRREFKS 211

RESULT 2
 S58875
 cdn-2 protein - human
 C:Species: Homo sapiens (man)
 C>Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 21-Jul-2000
 C:Accession: S58875
 R:Kiefer, M.C.; Brauer, M.J.; Powers, V.C.; Wu, J.J.; Umansky, S.R.; Tomei, L.D.; Barr,
 Nature 374, 736-739, 1995
 A:Title: Modulation of apoptosis by the widely distributed Bcl-2 homologue Bak.
 A:Reference number: S58874; MUID:95231654; PMID:7715731
 A:Accession: S58875
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-211 <KIE>
 A:Cross-references: EMBL:U16812; NID:9595925; PIDN:AA74467.1; PID:9595926
 A>Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1994

Query Match 97.5%; Score 1075; DB 2; Length 211;
 Best Local Similarity 97.2%; Pred. No. 7.8e-91;
 Matches 205; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Oy 1 MASGGGPPRROEGCEPALPSASEQVAQDTEEVFRSYVYRHOQEOAEVAPADPEM 60
 Db 1 MASGGGPPRROEGCEPALPSASEQVAQDTEEVFRSYVYRHOQEOAEVAPADPEM 60
 Oy 61 VTLPLQPSSTMGQVGRQALAIIGDDINRRYDSEFOTMLQLOPTAENAYEFTKATSLFE 120
 Db 61 VTLPLQPSSTMGQVGRQALAIIGDDINRRYDSEFOTMLQLOPTAENAYEFTKATSLFE 120
 Oy 121 SGINMGKRVALLGGRRLALHYQHGLTGFLGQVTRFVYDMLHHCIAIRWIAQRGWAA 180
 Db 121 SGINMGKRVALLGGRRLALHYQHGLTGFLGQVTRFVYDMLHHCIAIRWIAQRGWAA 180
 Oy 181 LNLGNGPILNLVVLGVLLGQFVVRREFKS 211
 Db 181 LNLGNGPILNLVVLGVLLGQFVVRREFKS 211

RESULT 3
 TYHUB1
 transforming protein bcl-2, splice form beta - human
 N:Alternate names: apoptosis regulator bcl-2
 C:Species: Homo sapiens (man)
 C>Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 15-Oct-1999
 C:Accession: B29409; I52566; D37332
 R:Tsujiimoto, Y.; Croce, C.M.
 Proc. Natl. Acad. Sci. U.S.A. 83, 5214-5218, 1986
 A:Title: Analysis of the structure, transcripts, and protein products of bcl-2, the gene
 A:Reference number: A29409; MUID:86259760; PMID:3523487
 A:Accession: B29409
 A:Molecule type: mRNA
 A:Residues: 1-205 <TSU>
 A:Cross-references: GB:M13995; NID:9179368; PIDN:AA51814.1; PID:9179369
 R:Tanaka, S.; Louie, D.C.; Kant, J.A.; Reed, J.C.
 Blood 79, 229-237, 1992
 A:Title: Frequent incidence of somatic mutations in translocated BCL2 oncogenes of non-H
 A:Reference number: I52566; MUID:92096610; PMID:1339299
 A:Accession: I52566
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-131 <TAN>
 A:Cross-references: GB:S72602; NID:9241046; PIDN:AD14111.1; PID:94261811
 R:Eguchi, Y.; Ewert, D.L.; Tsujiimoto, Y.
 Nucleic Acids Res. 20, 4187-4192, 1992
 A:Title: Isolation and characterization of the chicken bcl-2 gene: expression in a varie
 A:Reference number: A37332; MUID:92375724; PMID:1508712

A:Accession: D37332
 A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual
 A:Molecule type: DNA
 A:Residues: 1-33, 'E', 34-95, 'T', 97-109, 'R', 111-205 <EGU>
 C:Genetics:
 A:Gene: GDB:BCL2
 A:Cross-references: GDB:119031; OMIM:151430
 A:Map position: 18q21.3-18q21.3
 C:Function:
 A:Description: blocks apoptosis in hematopoietic cells
 C:Superfamily: bcl transforming protein
 C:Keywords: alternative splicing; apoptosis; B-cell lymphoma; follicular lymphoma; pr

Query Match 17.2%; Score 189.5; DB 1; Length 205;
 Best Local Similarity 27.4%; Pred. No. 6.6e-10;
 Matches 54; Conservative 27; Mismatches 73; Indels 43; Gaps 7;

Oy 30 DPEVFRSYVFRHQO---EQANEGV-----AANA-----DPEWVT 62
 Db 10 DNEIWMKTIHYKLSQGYEMDAGVGAAPGAPRPGIFSSQPGHTHPAASRPVART 69
 Oy 63 LPLO-PSSTMGQVGRQALAI-----GDDINRRYDSEFOTMLQLOPTAENAYEY 110
 Db 70 SPLQTPAAAGAAAPALSPVPVYHALNLQAGDDPSRRYRGDFAMSSQLHTPTARGR 129
 Oy 111 FKRIATSLFESGINMGKRVALLGGRRLALHYQHGLTGFLGQVTRFVYDMLHHCIAIRW 170
 Db 130 FATVVEELFRDGVNMGRIAVAFEEFGVMCVESVNRMSPLVDNALMMTEYLNRH-LHTW 188
 Oy 171 IAGRGWVAA---LNLG 184
 Db 189 IDPNGWVGASGDVSLG 205

RESULT 4
 TYHUB1
 transforming protein bcl-2, splice form alpha - human
 C:Species: Homo sapiens (man)
 C>Date: 31-Dec-1988 #sequence_revision 07-Jun-1996 #text_change 15-Oct-1999
 C:Accession: C37332; A29409; S02452; A24428; A27622; B27622
 R:Eguchi, Y.; Ewert, D.L.; Tsujiimoto, Y.
 Nucleic Acids Res. 20, 4187-4192, 1992
 A:Title: Isolation and characterization of the chicken bcl-2 gene: expression in a va
 A:Reference number: A37332; MUID:92375724; PMID:1508712
 A:Accession: C37332
 A:Status: nucleic acid sequence not shown; not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 1-239 <EGU>
 A>Note: this report is a correction
 R:Tsujiimoto, Y.; Croce, C.M.
 Proc. Natl. Acad. Sci. U.S.A. 83, 5214-5218, 1986
 A:Title: Analysis of the structure, transcripts, and protein products of bcl-2, the g
 A:Reference number: A29409; MUID:86259760; PMID:3523487
 A:Accession: A29409
 A:Molecule type: mRNA
 A:Residues: 1-95, 'A', 97-109, 'G', 111-236, 'S', 238-239 <TSU>
 A:Cross-references: GB:M13994; NID:9179366; PIDN:AA51813.1; PID:9179367
 A>Note: this sequence has been corrected in reference A37332
 R:Seto, M.; Jaeger, U.; Hockett, R.D.; Graninger, W.; Bennett, S.; Goldman, P.; Korsm
 EMBO J. 7, 123-131, 1988
 A:Title: Alternative promoters and exons, somatic mutation and deregulation of the Bc
 A:Reference number: S02452; MUID:88196071; PMID:2834197
 A:Accession: S02452
 A:Molecule type: mRNA
 A:Residues: 1-239 <SET>
 R:Cleary, M.L.; Smith, S.D.; Sklar, J.
 Cell 47, 19-28, 1986
 A:Title: Cloning and structural analysis of cDNAs for bcl-2 and a hybrid bcl-2/immuno
 A:Reference number: A24428; MUID:87002488; PMID:2875799
 A:Accession: A24428
 A:Molecule type: mRNA
 A:Residues: 1-58, 'T', 60-116, 'R', 118-239 <CLE>
 A:Cross-references: GB:M14745; NID:9179370; PIDN:AA35591.1; PID:9179371

R;Hua, C.; Zorn, S.; Jensen, J.P.; Coupland, R.W.; Ko, H.S.; Wright, J.J.; Bakshi, A.
 Oncogene Res. 2, 263-275, 1988
 A:Title: Consequences of the t(14;18) chromosomal translocation in follicular lymphoma:
 A:Reference number: A27622; MUID:86217344; PMID:3285301
 A:Accession: A27622
 A:Molecule type: mRNA
 A:Residues: 1-58, 'T', 60-239 <HUA>
 A:Accession: B27622
 A:Molecule type: DNA
 A:Residues: 1-6, 'S', 8-58, 'T', 60-128, 'C', 130-239 <HUA>
 A:Note: the sequence was determined from the germline gene
 C:Comment: Constitutive expression of Bcl2 following t(14;18) chromosomal translocation
 C:Gene: GDB:BCL2
 A:Cross-references: GDB:119031; OMIM:151430
 A:Map position: 18q21.3-18q21.3
 C:Function:
 A:Description: blocks apoptosis in hematopoietic cells
 C:Superfamily: bcl transforming protein
 C:Keywords: alternative splicing; apoptosis; B-cell lymphoma; follicular lymphoma; proto

Query Match 17.1%; Score 189; DB 1; Length 239;
 Best Local Similarity 26.4%; Pred. No. 8.9e-10;
 Matches 58; Conservative 31; Mismatches 81; Indels 50; Gaps 8;

QY 30 DTEEVRSYVFRHQQ---EQAEQV-----AAPA-----DPEMYT 62
 Db 10 DNEIYWKXTHYKLSRGYEMDAGVGAAPGAPAFISOPGHTPHPAASRDVART 69
 QY 63 LPLQ-PSSTMGVGRQLATII-----GDDINRRDSEFQTMLOHQAENAYEY 110
 Db 70 SPLQPAAGAAAGPALSVPPVHLLTQAGDPSRKRRDPAEKSSQLHTPTPTARG 129
 QY 111 FPKIATSEESGIMGRVVALGFGYRLAHYQHGLTGFLGQVTRFVDFMLHCICARW 170
 Db 130 FATVVEELFRDGVNMGRIYAFEEFGVMCESVNREMSPLVDNIALMTEYINRH-LHTW 188

QY 171 IAORGWVALNIGNPI-----LNVLVLGAVLLG 201
 Db 189 IDNGGMDAFVEL-YGFSMRPLFDPSWLSLKTLLSLALVG 227

RESULT 5
 A37332
 transforming protein (bcl-2-alpha) - chicken
 C:Species: Gallus gallus (chicken)
 C:Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 23-Feb-1997
 C:Accession: A37332; S35453
 R;Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.
 Nucleic Acids Res. 20, 4187-4192, 1992
 A:Title: Isolation and characterization of the chicken bcl-2 gene: expression in a varie
 A:Reference number: A37332; MUID:92375724; PMID:1508712
 A:Accession: A37332
 A:Status: nucleic acid sequence not shown
 A:Molecule type: DNA
 A:Residues: 1-233 <EGU>
 A:Cross-references: EMBL:DL1381
 C:Genetics:
 A:Introns: 189/3
 C:Superfamily: bcl transforming protein
 C:Keywords: mitochondrion; transforming protein; transmembrane protein

Query Match 16.6%; Score 183.5; DB 2; Length 233;
 Best Local Similarity 26.9%; Pred. No. 2.7e-09;
 Matches 57; Conservative 35; Mismatches 87; Indels 33; Gaps 10;

QY 2 ASGGC-PGPRRCGCEPALPSASEOVADTEEVRSYVFRHQQAEAGVAAAPADPE 59
 Db 31 AAGEDRPVPV-----APA-PAAPAAVA-----AAGASSHHRPEPPGSAASEVPPA 77
 QY 60 MVTPLQPSSTMGVGRQLAI--IGDDINRRDSEFQTMLOHQAENAYEYFTKATIS 117
 Db 78 EGLRPPV-----GVHLLRQAGDEFSSRRYORDFAQMSGQLHTLPTTAHGRFAVVEE 130

QY 118 LFESGIMGRVVALGFGYRLAHYQHGLTGFLGQVTRFVDFMLHCICARWITQRGW 177
 Db 131 LFRDGVNMGRIYAFEEFGVMCESVNREMSPLVDNIALMTEYINRH-LHNMIDNGW 189

QY 178 VALNL-GNG--PI-----LNVLVLGAVLLG 201
 Db 190 DAFVELYGNMRPLFDPSWLSLKTLLSLVVG 221

RESULT 6
 bcl-x long - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Jul-1999
 C:Accession: I49056; S52866
 R;Fang, W.; Rivard, J.J.; Mueller, D.L.; Behrens, T.W.
 J. Immunol. 153, 4388-4398, 1994
 A:Title: Cloning and molecular characterization of mouse bcl-x in B and T lymphocytes
 A:Reference number: I49055; MUID:95052604; PMID:7963517
 A:Accession: I49056
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-233 <RES>
 A:Cross-references: EMBL:U10101; NID:9506647; PIDN:AAA82173.1; PID:9506648
 submitted to the EMBL Data Library, November 1994
 A:Description: IL-5 inhibits anti-IgM-induced apoptosis in an immature B cell line th.
 A:Reference number: S52866
 A:Accession: S52866
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-233 <RAM>
 A:Cross-references: EMBL:X83574; NID:9695622; PIDN:CAA58557.1; PID:9695623
 C:Superfamily: bcl transforming protein

Query Match 16.4%; Score 181; DB 2; Length 233;
 Best Local Similarity 28.3%; Pred. No. 4.7e-09;
 Matches 43; Conservative 23; Mismatches 70; Indels 16; Gaps 3;

QY 71 MGQVROLATIGDDINRRDSEFQTMLOHQAENAYEYFTKATISLFSGIMGRVVA 130
 Db 83 MAAVKQALREAGDEFLRYRASFSLTSQLHTPTGAYQFQGVNLEFQGVNMGRIYA 142

QY 131 LFGYRLAHYQHGLTGFLGQVTRFVDFMLHCICARWITQRGWITNL-GNG-- 187
 Db 143 FFSFGALCYESVDKEQVLYSRASWMAIYLDH-LEPWIDNGWDFVVDLYGNMAA 201

QY 188 -----LNVLVLGAVVLLGQFVVR 207
 Db 202 ESRKQDERFNRMFLLTGWTAGVVLGSLFSRK 233

RESULT 7
 BCL-X protein - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 02-Mar-2001
 C:Accession: S51761; S51762
 R;Michaelidis, T.M.
 submitted to the EMBL Data Library, November 1994
 A:Reference number: S51761
 A:Accession: S51761
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-233 <MIC>
 A:Cross-references: EMBL:X82537; NID:9607176; PIDN:CAA57886.1; PID:9607177
 A:Experimental source: embryonic; Brain
 A:Accession: S51762
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-125, 189-233 <MI2>
 A:Cross-references: EMBL:X82537; NID:9607176; PIDN:CAA57887.1; PID:9607178

QY 75 GROLAI-----IGDDINRRYDSEFOTMLQHLPATAE 105
 Db 62 HREMAARTSPRLPVLATAGPALSPVPCVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTF 121
 QY 106 NAVEFTIATSLFESGIMNGRVALLGFGRLALHYQHGLTGFLGQVTRFVDEMLHH 165
 Db 122 TARGFAATVEELFEDGVMWGRIYAFEEFGVMCVESVNRKMSPLVDNIALMTEYLNRH 181
 QY 166 CIARWIAORGWVAALNLGNGPI-LNVL 192
 Db 182 -LHTWIDNGGWDFAVEL-YGPSMRPL 206

RESULT 11

153744
 gene bcl-2 protein - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 16-Jul-1999
 C:Accession: I53744
 R:Sato, T.; Irie, S.; Krajewski, S.; Reed, J.C.
 Gene 140, 291-292, 1994
 A:Title: Cloning and sequencing of a cDNA encoding the rat Bcl-2 protein.
 A:Reference number: I53744; MUID:94193015; PMID:8144041
 A:Accession: I53744
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-236 <RES>
 A:Cross-references: GB:I44680; NID:g408946; PIDN:AAA53662.1; PID:g408947
 C:Genetics:
 A:Gene: bcl-2
 C:Superfamily: bcl transforming protein

Query Match 16.0%; Score 176.5; DB 2; Length 236;
 Best Local Similarity 24.2%; Pred. No. 1.2e-08;
 Matches 55; Conservative 31; Mismatches 90; Indels 51; Gaps 7;

QY 22 ASEQVADTEEVFRSYFYRHQ-----EQBAEVAAPA----- 56
 Db 2 AAGGTGYNREIVKTYHKLISQGYEMDTGDDSDAPLRAAPPGIFSFQPESENRPAY 61
 QY 57 --DEPMVTLPLQPSSTMGVGRQALII-----GDDINRRYDSEFOTMLQHLP 103
 Db 62 HRDIAARTSPRLP--LVANAGPALSPVPPVHLLRRAGDDFSRRYRRDFAEMSSQLHLT 119
 QY 104 AENAVEFTKATSLFESGIMNGRVALLGFGRLALHYQHGLTGFLGQVTRFVDEML 163
 Db 120 PFTARGFAATVEELFEDGVMWGRIYAFEEFGVMCVESVNRKMSPLVDNIALMTEYL 179
 QY 164 HHCIARWIAORGWVAALNLGNGPI-----LNVLVVLGVVLLG 201
 Db 180 RH-LHTWIDNGGWDFAVEL-YGPSMRPLFDFSWSLSTKLTLSTLALVG 224

RESULT 12

B37332
 transforming protein (bcl-2-beta) - chicken
 C:Species: Gallus gallus (chicken)
 C>Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 24-Apr-1998
 C:Accession: B37332; S35452
 R:Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.
 Nucleic Acids Res. 20, 4187-4192, 1992
 A:Title: Isolation and characterization of the chicken bcl-2 gene: expression in a variety of tissues.
 A:Reference number: A37332; MUID:92375724; PMID:1508712
 A:Accession: B37332
 A>Status: nucleic acid sequence not shown
 A:Molecule type: DNA
 A:Residues: 1-216 <REGU>
 A:Cross-references: EMBL:DJ1381; EMBL:DJ1382
 C:Superfamily: bcl transforming protein

Query Match 15.8%; Score 174.5; DB 2; Length 216;
 Best Local Similarity 27.3%; Pred. No. 1.7e-08;
 Matches 50; Conservative 27; Mismatches 81; Indels 25; Gaps 7;

QY 2 ASGCG--PG3PROECGPALPSASEEYVADTEEVFRSYFYRHQOEAEVAAPADE 59
 Db 31 AAGEDRPPVP-----APA-PAAPAAVA-----AAGASHHREPPSAAASEVPA 77
 QY 60 MVTPLPLQPSSTMGVGRQALII-----IGDDINRRYDSEFOTMLQHLPANAVEFTIAT 117
 Db 78 EGLRAPFP-----GVHLLARQAGDEFSSRRYQRDRQMSGQLHLPFAHGFVAVEE 130
 QY 118 LFESGIMNGRVALLGFGRLALHYQHGLTGFLGQVTRFVDEMLHHCIARWIAORGW 177
 Db 131 LFRDGVNMGRIYAFEEFGVMCVESVNRKMSPLVDNIALMTEYLNRH-LHNWIDNGGM 189

RESULT 13

167431
 BCL-X-Long - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 16-Jul-1999
 C:Accession: I67431
 R:Tilly, J.L.; Tilly, K.L.; Kenton, M.L.; Johnson, A.L.
 Endocrinology 136, 232-241, 1995
 A:Title: Expression of members of the bcl-2 gene family in the immature rat ovary: eq
 onstitutive bcl-2 and bcl-x-long messenger ribonucleic acid levels.
 A:Reference number: I53295; MUID:95129487; PMID:7828536
 A:Accession: I67431
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-233 <RES>
 A:Cross-references: EMBL:U34963; NID:g1004376; PIDN:AAA77686.1; PID:g1004377
 C:Superfamily: bcl transforming protein

Query Match 15.7%; Score 173.5; DB 2; Length 233;
 Best Local Similarity 27.6%; Pred. No. 2.3e-08;
 Matches 48; Conservative 25; Mismatches 78; Indels 23; Gaps 5;

QY 49 AEGVAPADPEMTPLPLQPSSTMGVGRQALIIIGDDINRRYDSEFOTMLQHLPANAY 108
 Db 68 ATGHSSSLAREV-LP-----MAAVKQALREAGDEFELRYRRASDLTSQHLTPGYV 120
 QY 109 EYFTKATSLFESGIMNGRVALLGFGRLALHYQHGLTGFLGQVTRFVDEMLHHCIA 168
 Db 121 QSEQVYNELFRDGVNMGRIYAFSSFGALCVESVDKEMQVLSKASMAATYLNDR-LE 179
 QY 169 RWIAORGWVAALNLGNGP-----ILNVLVVLGVVLLGQFVVR 207
 Db 180 PWIOENGWMDTFVDLYGNNTAPESRKGERFNRWFLTGWTVAGVYLLGSLPSRK 233

RESULT 14

JC7383
 B-cell lymphoma 2 protein - Chinese hamster
 C:Species: Cricetus griseus (Chinese hamster)
 C>Date: 17-Nov-2000 #sequence_revision 17-Nov-2000 #text_change 08-Dec-2000
 C:Accession: JC7383
 R:Tomicic, M.T.; Christmann, M.; Kaina, B.
 Biochem. Biophys. Res. Commun. 275, 899-903, 2000
 A:Title: Cloning and functional analysis of cDNA encoding the hamster Bcl-2 protein.
 A:Reference number: JC7383
 A:Accession: JC7383
 A:Contents: Ovary

A:Molecule type: mRNA
 A:Residues: 1-236 <TOM>
 A:Cross-references: GB:A1271720
 C:Comment: This protein has anti-apoptotic function, and supports cell survival.
 C:Genetics:
 A:Gene: bcl-2
 C:Superfamily: bcl transforming protein
 C:Keywords: B-cell lymphoma; ovary

GenCore version 5.1.4.P5.4578
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OM protein - protein search, using sw model

Run on: March 27, 2003, 10:44:38 ; Search time 13 Seconds

(Without alignments)
673.193 Million cell updates/sec

Title: US-09-633-200-7

Perfect score: 1103
Sequence: 1 MASGGGPPROEGGEPALP.....LWLVGVLLGFFVRRFFKS 211

Scoring table: BLOSUM62

Gapop 10.0 , Capext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1103	100.0	211	1	BAK_HUMAN
2	1075	97.5	211	1	BAK_HUMAN
3	829.5	75.2	208	1	BAK_MOUSE
4	189	17.1	239	1	BCI2_HUMAN
5	186	16.9	229	1	BCI2_BOVIN
6	184	16.7	229	1	BCI2_BOVIN
7	183.5	16.6	233	1	BCI2_CHICK
8	181	16.4	233	1	BCI2_MOUSE
9	181	16.4	233	1	BCI2_MOUSE
10	180	16.3	233	1	BCI2_MOUSE
11	179.5	16.3	236	1	BCI2_MOUSE
12	178.5	16.2	236	1	BCI2_MOUSE
13	176	16.0	193	1	BCI2_MOUSE
14	176	16.0	233	1	BCI2_MOUSE
15	172.5	15.6	204	1	AR11_XENLA
16	172.5	15.6	236	1	BCI2_CRILLO
17	171	15.5	193	1	BCI2_MOUSE
18	159	14.4	228	1	AR1_XENLA
19	146	13.2	218	1	BAKX_HUMAN
20	143	13.0	192	1	BAKX_HUMAN
21	143	13.0	192	1	BAKX_HUMAN
22	141.5	12.8	350	1	MCL1_HUMAN
23	141	12.8	192	1	BAKX_MOUSE
24	134	12.1	192	1	BAKX_MOUSE
25	116	10.5	172	1	BFL1_MOUSE
26	112	10.2	175	1	BFL1_MOUSE
27	109	9.9	143	1	BAKX_HUMAN
28	107.5	9.7	177	1	BAKX_HUMAN
29	97	8.8	892	1	NR13_CORJA
30	86	7.8	179	1	SVL_PYRAE
31	85.5	7.8	1237	1	EAR_ASPE4
32	85	7.7	179	1	EAR_ASPE4
33	84	7.6	179	1	EAR_ASPE4

34	81.5	7.4	742	1	SUN2_HUMAN	Q9uh99 homo sapien
35	81.5	7.4	757	1	DRA_RAT	Q924c9 rattus norv
36	81	7.3	1238	1	B3A2_CAVPO	0920s8 cavia porce
37	80.5	7.3	244	1	CAH_ERMCA	052538 erwinta car
38	80.5	7.3	420	1	YO20_BACHD	Q9ka70 bacillius ha
39	80	7.3	133	1	GOP_BPp4	P13058 bacterioph
40	80	7.3	911	1	B3AT_HUMAN	P97738 rattus norv
41	79.5	7.2	432	1	NPX2_RAT	P02730 homo sapien
42	79.5	7.2	1234	1	B3A2_RAT	P97738 rattus norv
43	79	7.2	427	1	APEX_CAVPO	P47970 cavia porce
44	79	7.2	469	1	MENE_LISIN	Q92ay8 listeria in
45	79	7.2	498	1	IDHP_ASFNG	P79089 aspergillus

ALIGNMENTS

RESULT 1	BAK_HUMAN	STANDARD;	PRT;	211 AA.
AC	Q16611; Q92533;			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Bcl-2 homologous antagonist/killer (Apoptosis regulator BAK).			
GN	BAK1 OR BAK.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=B-cell.			
RX	MEDLINE=95231652; PubMed=7715729;			
RA	Farrow S.N., White J.H.M., Martinou I., Raven T., Pun K.-T.,			
RA	Grimham C.J., Martinou J.C., Brown R.;			
RT	"Cloning of a bcl-2 homologue by interaction with adenovirus E1B			
RT	19K.";			
RL	Nature 374:731-733(1995).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=95231653; PubMed=7715730;			
RA	Chittenden T., Harrington E.A., O'Connor R., Flemington C., Lutz R.J.,			
RA	Evan G.I., Guild B.C.;			
RT	"Induction of apoptosis by the Bcl-2 homologue Bax.";			
RL	Nature 374:733-736(1995).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=95231654; PubMed=7715731;			
RA	Kiefer M.C., Brauer M.J., Powers V.C., Wu J.J., Umansky S.R.,			
RA	Tomei L.D., Barr P.J.;			
RT	"Modulation of apoptosis by the widely distributed Bcl-2 homologue			
RT	Bax.";			
RL	Nature 374:736-739(1995).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RA	Williams S.;			
RL	Submitted (Jan-2000) to the EMBL/GenBank/DBJ databases.			
RP	[5]			
RP	SEQUENCE OF 96-206 FROM N.A.			
RA	Eguchi H., Hayashi S.;			
RL	Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.			
RN	[6]			
RP	MOTAGENESIS, AND FUNCTION OF BH3 DOMAIN.			
RX	MEDLINE=96091131; PubMed=8521816;			
RA	Chittenden T., Flemington C., Houghton A.B., Ebb R.G., Gallo G.J.,			
RA	Elangovan B., Chinnadurai G., Lutz R.J.;			
RT	"A conserved domain in Bax, distinct from BH1 and BH2, mediates cell			
RT	death and protein binding functions.";			
RL	EMBO J. 14:5589-5596(1995).			
RN	[7]			
RP	STRUCTURE BY NMR OF 72-87.			
RX	MEDLINE=97172562; PubMed=9020082;			

RA Sattler M., Liang H., Nettesheim D., Meadows R.P., Harlan J.E.,
RA Eberstadt M., Yoon H.S., Shuker S.B., Chang B.S., Minn A.J.,
RA Thompson C.B., Pesik S.W.,
RT Structure of Bcl-XL-Bak peptide complex: recognition between
RT regulators of apoptosis.";
RL Science 275:983-986(1997).
CC -1- FUNCTION: IN THE PRESENCE OF AN APPROPRIATE STIMULUS, ACCELERATES
CC PROGRAMMED CELL DEATH BY BINDING TO, AND ANTAGONIZING THE A
CC REPRESSOR BCL-2 OR ITS ADENOVIRUS HOMOLOG E1B 19K PROTEIN.
CC -1- SUBUNIT: FORMS HETERODIMERS WITH BCL-2, E1B 19K PROTEIN, AND BCL-
CC X(L).
CC -1- SUBCELLULAR LOCATION: Membrane-bound (potential).
CC -1- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES, WITH
CC HIGHEST LEVELS IN THE HEART AND SKELETAL MUSCLE.
CC -1- DOMAIN: INTACT BH3 DOMAIN IS REQUIRED BY BIK, BID, BAK, BAD AND
CC BAX FOR THEIR PRO-APOPTOTIC ACTIVITY AND FOR THEIR INTERACTION
CC WITH ANTI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.
CC APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
DR EMBL: X84213; CAA58997.1; -;
DR EMBL: U23765; AAA93066.1; -;
DR EMBL: U16811; AAA74466.1; -;
DR EMBL: Z93017; CAB5626.1; -;
DR EMBL: D88397; BAA13606.1; -;
DR EMBL: D88396; BAA13606.1; JOINED.
DR PDB: 1BXL; 29-OCT-97.
DR Genew: HGNC:949; BAK1.
DR MIM: 600516; -;
DR InterPro: IPR002475; BCL2_family.
DR InterPro: IPR000712; BCL2_BH.
DR Pfam: PF00452; BCL-2; 1.
DR SMART: SM00337; BCL; 1.
DR PROSITE: PS01080; BH1; 1.
DR PROSITE: PS01258; BH2; 1.
DR PROSITE: PS01259; BH3; 1.
DR PROSITE: PS50062; BCL2_FAMILY; 1.
DR Apoptosis; Transmembrane; 3D-structure.
KW Apoptosis; Transmembrane; 3D-structure.
FT DOMAIN 74 88 BH3.
FT DOMAIN 117 136 BH1.
FT DOMAIN 169 184 BH2.
FT TRANSMEM 188 205 POTENTIAL.
SQ SEQUENCE 211 AA; A2200E72A46D04E CMC64;

Query Match 100.0%; Score 1103; DB 1; Length 211;
Best Local Similarity 100.0%; Pred. No. 6, 2e-92;
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 181 LNLGNGPILNVLVGLGVLLGQFVVRFFKS 211

RESULT 2
BAK2_HUMAN STANDARD; PRT; 211 AA.
AC Q13014;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Bcl-2 homologous antagonist/killer 2 (Apoptosis regulator BAK-2).
GN BCL2L7P1 (Human).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95231654; PubMed=7715731;
RA Kiefer M.C., Brauer M.J., Powers V.C., Wu J.J., Umansky S.R.,
RA Tomei L.D., Barr P.J.;
RT "Modulation of apoptosis by the widely distributed Bcl-2 homologue
RT Bak-2".
RL Nature 374:736-739(1995).
CC -1- FUNCTION: IN THE PRESENCE OF AN APPROPRIATE STIMULUS, ACCELERATES
CC PROGRAMMED CELL DEATH BY BINDING TO, AND ANTAGONIZING THE A
CC REPRESSOR BCL-2 OR ITS ADENOVIRUS HOMOLOG E1B 19K PROTEIN.
CC -1- SUBUNIT: FORMS HETERODIMERS WITH BCL-2, E1B 19K PROTEIN, AND BCL-
CC X(L).
CC -1- SUBCELLULAR LOCATION: Membrane-associated (potential).
CC -1- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES, WITH
CC HIGHEST LEVELS IN THE HEART AND SKELETAL MUSCLE.
CC -1- DOMAIN: INTACT BH3 DOMAIN IS REQUIRED BY BIK, BID, BAK, BAD AND
CC BAX FOR THEIR PRO-APOPTOTIC ACTIVITY AND FOR THEIR INTERACTION
CC WITH ANTI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.
CC APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC -1- CAUTION: THIS COULD BE THE PRODUCT OF A PSEDOGENE.
CC -----
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CC -----
DR EMBL: U16812; AAA74467.1; -;
DR HSP: Q16811; 1BXL.
DR Genew: HGNC:996; BCL2L7P1.
DR InterPro: IPR002475; BCL2_family.
DR InterPro: IPR000712; BCL2_BH.
DR Pfam: PF00452; BCL-2; 1.
DR SMART: SM00337; BCL; 1.
DR PROSITE: PS01080; BH1; 1.
DR PROSITE: PS01258; BH2; 1.
DR PROSITE: PS01259; BH3; 1.
DR PROSITE: PS50062; BCL2_FAMILY; 1.
DR Apoptosis; Transmembrane.
KW Apoptosis; Transmembrane.
FT DOMAIN 74 88 BH3.
FT DOMAIN 117 136 BH1.
FT DOMAIN 169 184 BH2.
FT TRANSMEM 188 205 POTENTIAL.
SQ SEQUENCE 211 AA; 703875EC4DCCCB3 CMC64;

Query Match 97.5%; Score 1075; DB 1; Length 211;
Best Local Similarity 97.2%; Pred. No. 2e-89;
Matches 205; Conservative 2; Mismatches 4; Indels 0; Gaps 0;


```

Db 1 MASGGGPPRQECGPALPSASEQVADTEEFVFRSVFTHHQOEBAQAAAPADPEM 60
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Db 61 VTLPLOPSSTMGQVGRQALITGDDINRRYDSEFQTMLOHPTAENAYEFTKIATSLFE 120
QY 121 SGIMNGRVALLGEGYRLALHYOHGLTGLGQVTRFVVDPMHHCIAIRIAQRGWVAA 180
Db 121 SGIMNGRVALLGEGYRLALHYOHGLTGLGQVTRFVVDPMHHCIAIRIAQRGWVAA 180
QY 181 LNLGNGPILNVLVGLVGLGQFVVRREFKS 211
Db 181 LNLGNGPILNVLVGLVGLGQFVVRREFKS 211

RESULT 3
BAK_MOUSE
ID BAK_MOUSE STANDARD; PRT; 208 AA.
AC 008734;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Bcl-2 homologous antagonist/killer (Apoptosis regulator BAK).
GN BAK1 OR BAK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Swiss; TISSUE=Liver;
RX MEDLINE=97446138; PubMed=9299236;
RA Ulrich E., Kaufmann-Zeh A., Hueber A.O., Williamson J.,
RA Chittenden T., Ma A., Evan G.I.;
RT "Gene structure, cDNA sequence, and expression of murine Bak, a
RT proapoptotic Bcl-2 family member.";
RL Genomics 44:195-200(1997).
CC -1- FUNCTION: IN THE PRESENCE OF AN APPROPRIATE STIMULUS, ACCELERATES
CC PROGRAMMED CELL DEATH BY BINDING TO, AND ANTAGONIZING THE A
CC REPRESSOR BCL-2 OR ITS ADENOVIRUS HOMOLOG E1B 19K PROTEIN (BY
CC SIMILARITY).
CC -1- SUBUNIT: FORMS HETERODIMERS WITH BCL-2, E1B 19K PROTEIN, AND BCL-
CC X(L) (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Membrane-associated (Potential).
CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED.
CC -1- DOMAIN: INTACT BH3 DOMAIN IS REQUIRED BY BIK, BID, BAK, BAD AND
CC BAX FOR THEIR PRO-APOPTOTIC ACTIVITY AND FOR THEIR INTERACTION
CC WITH ANTI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.
CC APOPTOTIC MEMBERS OF THE BCL-2 FAMILY (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation-
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: Y13331; CAA73684.1; -
DR HSSP: Q16611; 1BXL.
DR MGD: MGI:1097161; Bak1
DR InterPro: IPR002475; BCL2_family.
DR InterPro: IPR000712; BCL2_BH.
DR Pfam: PF00452; Bcl-2; 1.
DR SMART: SM00337; BCL; 1.
DR PROSITE: PS01080; BH1; 1.
DR PROSITE: PS01258; BH2; 1.
DR PROSITE: PS01259; BH3; 1.

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DR PROSITE: PS00062; BCL2_FAMILY; 1.
KW Apoptosis; Transmembrane.
FT DOMAIN 71 85 BH3.
FT DOMAIN 114 133 BH1.
FT DOMAIN 166 181 BH2.
FT TRANSMEM 185 202 POTENTIAL.
SQ SEQUENCE 208 AA; 23300 MW; DAFCL1B160C523C9 CRC64;

Query Match 75.28; Score 829.5; DB 1; Length 208;
Best Local Similarity 76.38; Pred. No. 2,1e-67;
Matches 161; Conservative 20; Mismatches 27; Indels 3; Gaps 2;

QY 1 MASGGGPPRQECGPALPSASEQVADTEEFVFRSVFTHHQOEBAQAAAPADPEM 60
Db 1 MASGGGPPRQECGPALPSASEQVADTEEFVFRSVFTHHQOEBAQAAAPADPEM 60
QY 61 VTLPLOPSSTMGQVGRQALITGDDINRRYDSEFQTMLOHPTAENAYEFTKIATSLFE 120
Db 61 VTLPLOPSSTMGQVGRQALITGDDINRRYDSEFQTMLOHPTAENAYEFTKIATSLFE 120
QY 58 DNLPLEPNSILGQVGRQALITGDDINRRYDSEFQTMLOHPTAENAYEFTKIATSLFE 117
Db 58 DNLPLEPNSILGQVGRQALITGDDINRRYDSEFQTMLOHPTAENAYEFTKIATSLFE 117
QY 121 SGIMNGRVALLGEGYRLALHYOHGLTGLGQVTRFVVDPMHHCIAIRIAQRGWVAA 180
Db 121 SGIMNGRVALLGEGYRLALHYOHGLTGLGQVTRFVVDPMHHCIAIRIAQRGWVAA 180
QY 181 LNLGNGPILNVLVGLVGLGQFVVRREFKS 211
Db 181 LNLGNGPILNVLVGLVGLGQFVVRREFKS 211
Db 178 LNLGNGPILNVLVGLVGLGQFVVRREFKS 208

RESULT 4
BCL2_HUMAN
ID BCL2_HUMAN STANDARD; PRT; 239 AA.
AC P10415; P10416; Q16197; Q13842;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Apoptosis regulator Bcl-2.
GN BCL2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA AND BETA).
RX MEDLINE=86259760; PubMed=3523487;
RA Tsujimoto Y., Croce C.M.;
RT "Analysis of the structure, transcripts, and protein products of
RT bcl-2, the gene involved in human follicular lymphoma.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:5214-5218(1986).
RN [2]
RP REVISIONS TO 96: 110 AND 237.
RX MEDLINE=92375724; PubMed=1508712;
RA Eguchi Y., Ewert D.L., Tsujimoto Y.;
RT "Isolation and characterization of the chicken bcl-2 gene: expression
RT in a variety of tissues including lymphoid and neuronal organs in
RT adult and embryo.";
RL Nucleic Acids Res. 20:4187-4192(1992).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
RX MEDLINE=87002488; PubMed=2875799;
RA Cleary M.L., Smith S.D., Sklar J.;
RT "Cloning and structural analysis of cDNAs for bcl-2 and a hybrid bcl-
RT 2/immunoglobulin transcript resulting from the t(14;18)
RT translocation.";
RL Cell 47:19-28(1986).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
RX MEDLINE=86196071; PubMed=2834197;
RA Seto M., Jaeger U., Hockett R.D., Granger W., Bennett S.,
RA Goldman P., Koremeyer S.J.;
RT "Alternative promoters and exons, somatic mutation and deregulation
RT of the Bcl-2-ig fusion gene in lymphoma.";
RL EMBO J. 7:123-131(1988).

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RN [5] SEQUENCE OF 1-131 FROM N.A. (ISOFORM ALPHA), AND VARIANTS NHL.
 RP MEDLINE=92096610; PubMed=1339299;
 RX Tanaka S., Louie D.C., Kant J.A., Reed J.C.;
 RA "Frequent incidence of somatic mutations in translocated BCL2
 RT oncogenes of non-Hodgkin's lymphomas.";
 RL Blood 79:229-237(1992).
 RN [6]
 RP SUBCELLULAR LOCATION.
 RX MEDLINE=91066924; PubMed=2250705;
 RA Hockenbery D., Nunez G., Millman C., Schreiber R.D., Korsmeyer S.J.;
 RT "Bcl-2 is an inner mitochondrial membrane protein that blocks
 RT programmed cell death.";
 RL Nature 348:334-336(1990).
 RN [7]
 RP MUTAGENESIS.
 RX MEDLINE=94239528; PubMed=8183370;
 RA Yin X.-M., Oltvai Z.N., Korsmeyer S.J.;
 RT "Bhl and Bhl2 domains of Bcl-2 are required for inhibition of
 RT apoptosis and heterodimerization with Bax.";
 RL Nature 369:321-323(1994).
 RN [8]
 RP CLEAVAGE BY CASPASES, AND MUTAGENESIS.
 RX MEDLINE=98057466; PubMed=9395403;
 RA Cheng E.H.-Y., Kirsch D.G., Clem R.J., Ravi R., Kastan M.B., Bedi A.,
 RT Ueno K., Hardwick J.M.;
 RL "Conversion of Bcl-2 to a Bax-like death effector by caspases.";
 RL Science 278:1966-1968(1997).
 RN [9]
 RP REVIEW ON PHOSPHORYLATION.
 RX MEDLINE=21260650; PubMed=11368354;
 RA Kuvolo P.P., Deng X., May W.S.;
 RT "Phosphorylation of Bcl2 and regulation of apoptosis.";
 RL Leukemia 15:515-522(2001).
 RN [10]
 RP PHOSPHORYLATION BY ASK1/JNK1.
 RX MEDLINE=20036804; PubMed=10567572;
 RA Yamamoto K., Ichijo H., Korsmeyer S.J.;
 RT "Bcl-2 is phosphorylated and inactivated by an ASK1/Jun N-terminal
 RT protein kinase pathway normally activated at G(2)/M.";
 RL Mol. Cell. Biol. 19:8469-8478(1999).
 CC -1- FUNCTION: Suppresses apoptosis in a variety of cell systems
 CC including factor-dependent lymphohematopoietic and neural cells.
 CC Regulates cell death by controlling the mitochondrial membrane
 CC permeability. Appears to function in a feedback loop system with
 CC caspases. Inhibits caspase activity either by preventing the
 CC release of cytochrome c from the mitochondria and/or by binding to
 CC the apoptosis-activating factor (Apaf-1).
 CC -1- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and
 CC Bcl-x(L). Heterodimerization with BAX requires intact BHL and BHL2
 CC domains, and is necessary for anti-apoptotic activity (By
 CC similarity). Also interacts with APAF-1 and RAFL-1.
 CC -1- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular
 CC membrane of the nuclear envelope and the endoplasmic reticulum.
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; alpha (shown here) and beta;
 CC are produced by alternative splicing.
 CC -1- TISSUE SPECIFICITY: Expressed in a variety of tissues.
 CC -1- DOMAIN: The BHL domain is required for anti-apoptotic activity and
 CC for interaction with RAFL-1.
 CC -1- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2
 CC anti-apoptotic activity. Growth factor-stimulated phosphorylation
 CC on Ser-70 by PKC is required for the anti-apoptosis activity and
 CC occurs during the G2/M phase of the cell cycle. In the absence of
 CC growth factors, Bcl2 appears to be phosphorylated by other protein
 CC kinases such as ERKs and stress-activated kinases.
 CC -1- PTM: Proteolytically cleaved by caspases during apoptosis. The
 CC cleaved protein, lacking the BHL domain, has pro-apoptotic
 CC activity, causes the release of cytochrome c into the cytosol
 CC promoting further caspase activity.
 CC -1- DISEASE: Involved in follicular lymphoma (FL) (also known as type
 CC II chronic lymphatic leukemia) by a chromosomal translocation
 CC t(14;18)(q32;q21) which involves Bcl2 and immunoglobulin gene

CC regions.
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BHL) DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BHL2) DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BHL3) DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BHL4) DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 5 (BHL5) DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 6 (BHL6) DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 7 (BHL7) DOMAIN.
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DE Apoptosis regulator Bcl-X.
 GN BCL2L1 OR BCLX OR BCL-X.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 CC Gallus.
 NCBI_TaxID=9031;
 RX NCBI_TaxID=9031;
 RP SEQUENCE FROM N.A. (SHORT FORM).
 RA MEDLINE=93364977; PubMed=8358789;
 RA Bolse L.H., Gonzalez-Garcia M., Postema C.E., Ding L., Lindsten T.,
 RA Tuka L.A., Mao X., Nunez G., Thompson C.B.;
 RA "bcl-x, a bcl-2-related gene that functions as a dominant regulator
 RA of apoptotic cell death.";
 RA Cell 74:597-608(1993).
 RN [2]
 RN SEQUENCE FROM N.A. (LONG FORM).
 RC STRAIN=Hubbard White Mountain; TISSUE=Testis;
 RX MEDLINE=97264485; PubMed=9110311;
 RX Vilagrasa X., Mezquita C., Mezquita J.;
 RX "Differential expression of bcl-2 and bcl-x during chicken
 RX spermatogenesis.";
 RX Mol. Reprod. Dev. 47:26-29(1997).
 CC -1- FUNCTION: DOMINANT REGULATOR OF APOPTOTIC CELL DEATH. THE LONG
 CC FORM DISPLAYS CELL DEATH REPRESSOR ACTIVITY, WHEREAS THE SHORT
 CC ISOFORM PROMOTES APOPTOSIS (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR
 CC ENVELOPE (BY SIMILARITY).
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: A LONG FORM (SHOWN HERE) AND A
 CC SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN ORGANS WITH LYMPHOID
 CC DEVELOPMENT.
 CC -1- DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC
 CC FUNCTION. INTRAC BHL AND BH2 DOMAINS ARE REQUIRED FOR ANTI-
 CC APOPTOTIC ACTIVITY (BY SIMILARITY).
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.
 CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC -----
 CC EMBL; 223110; CAA80657.1; -;
 DR EMBL; 026645; AAB07677.1; -;
 DR PIR; A47537; A47537.
 DR HSSP; P53563; IAR3.
 DR InterPro; IPR002475; BCL2_family.
 DR InterPro; IPR000712; Bcl2_BH.
 DR InterPro; IPR003093; Bcl2_BH4.
 DR InterPro; IPR004725; Bcl2_reg.
 DR Pfam; PF00452; Bcl-2; 1.
 DR Pfam; PF02180; BH4; 1.
 DR SMART; SM00337; BCL; 1.
 DR SMART; SM00265; BH4; 1.
 DR TIGRfams; TIGR00865; bcl-2; 1.
 DR PROSITE; PS50062; BCL2_FAMILY; 1.
 DR PROSITE; PS01080; BH1; 1.
 DR PROSITE; PS01258; BH2; 1.
 DR PROSITE; PS01259; BH3; 1.
 DR PROSITE; PS01260; BH4_1; 1.
 DR PROSITE; PS50063; BH4_2; 1.
 KW Apoptosis; Transmembrane; Alternative splicing.
 FT DOMAIN 4 24
 FT DOMAIN 82 96 BH4.
 FT DOMAIN 125 144 BH3.
 FT DOMAIN 176 191 BH2.

FT TRANSMEM 206 223 POTENTIAL.
 FT VARSPIC 185 229 ERFVLDYGNNAAEIRKQETFNKMLTGATVAGVLLGSL
 FT SEQUENCE 229 AA: 25733 MW: A97D3A4D04C0E9DA CRC64;
 Query Match 16.7%; Score 184; DB 1; Length 229;
 Best Local Similarity 23.9%; Pred. No. 1.9e-09;
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 QY 27 VADTTEVFRRSYVFYRHOQ-----EQEAGC---VVAAPADPENV----- 61
 DB 1 MSSSNRELYIDFVSYKLSRGHCWSELEEDENRDTAAEAMDVYNGSPWHPAGHV 60
 QY 62 -----TLPLPSSSTGQVGRQALIGDDINRRYSEFQTMLOHLPAAENAYEFT 112
 DB 61 VNCATVHRSSLEHVELVRSADVQALRDAGDEFLRYRAFSDLRSQHLTPGTAYOSFE 120
 QY 113 KIATSLFESGINKGRVYVALLGFRALAHVYQHGTLGFGQVTRVYDFMLHICARMTA 172
 DB 121 QVYNELFHGQVNMGRIVAFESFGALCVBSVDKEMKRVIGRTVSMWTYLTDH-LDPWIQ 179
 QY 173 QREGVY-----AALNMGNGP-----ILNVVLGVLLGQFVYVR 207
 DB 180 ENGGWERFVDLYGNNAAEIRKQETFNKMLTGATVAGVLLGSLSRK 229
 RESULT 7
 BCL2_CHICK
 ID BCL2_CHICK STANDARD; PRT: 233 AA.
 AC 000709;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Apoptosis regulator Bcl-2.
 GN BCL2 OR BCL-2.
 OS Gallus gallus (Chicken).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 CC Gallus.
 NCBI_TaxID=9031;
 RX NCBI_TaxID=9031;
 RP SEQUENCE FROM N.A.
 RA MEDLINE=92375724; PubMed=1508712;
 RA Buchh Y., Ewert D.L., Tsujimoto Y.;
 RA "Isolation and characterization of the chicken bcl-2 gene: expression
 RA in a variety of tissues including lymphoid and neuronal organs in
 RA adult and embryo.";
 RA Nucleic Acids Res. 20:4187-4192(1992).
 RN [2]
 RN SEQUENCE FROM N.A.
 RC TISSUE=B-cell lymphoma;
 RX MEDLINE=92379084; PubMed=1511008;
 RA Cazals-Hatem D.L., Louie D.C., Tanaka S., Reed J.C.;
 RT "Molecular cloning and DNA sequence analysis of cDNA encoding chicken
 RT homologue of the Bcl-2 oncoprotein.";
 RL Biochim. Biophys. Acta 1132:109-113(1992).
 CC -1- FUNCTION: Suppresses apoptosis in a variety of cell systems
 CC including factor-dependent lymphohematopoietic and neural cells.
 CC Regulates cell death by controlling the mitochondrial membrane
 CC permeability. Appears to function in a feedback loop system with
 CC caspases. Inhibits caspase activity either by preventing the
 CC release of cytochrome c from the mitochondria and/or by binding to
 CC the apoptosis-activating factor (APAF-1).
 CC -1- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and
 CC Bcl-X(L). Heterodimerization with BAX requires intact BH1 and BH2
 CC domains, and is necessary for anti-apoptotic activity (By
 CC similarity). Also interacts with APAF-1 and RAIF-1 (By similarity).
 CC -1- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular
 CC membrane of the nuclear envelope and the endoplasmic reticulum.
 CC -1- TISSUE SPECIFICITY: In adult chicken expressed, in thymus, spleen,
 CC kidney, heart, ovary and brain, with the highest levels in the
 CC thymus. In the embryo, highly levels expressed in all tissues with
 CC high levels in the bursa of Fabricius.

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CC -1- DOMAIN: The Bcl-4 domain is required for anti-apoptotic activity and
CC for interaction with Raf-1 (By similarity).
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
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CC EMBL: D11382; BAA01978.1; -.
CC EMBL: D11381; BAA01978.1; JOINED.
CC EMBL: 211961; CA978018.1; -.
CC PIR: A37332; A37332.
CC PIR: S24390; S24390.
CC HSP: Q07817; IMAZ.
CC InterPro: IPR002475; BCL2 family.
CC InterPro: IPR000712; Bcl2_BH.
CC InterPro: IPR003093; Bcl2_BH4.
CC InterPro: IPR004725; Bcl2_reg.
CC Pfam: PF00452; Bcl-2; 1.
CC SMART: SM00337; BCL; 1.
CC SMART: SM00265; BH4; 1.
CC TIGRfam: TIGR00865; bcl-2; 1.
CC PROSITE: PS50062; BCL2_FAMILY; 1.
CC PROSITE: PS01080; BH1; 1.
CC PROSITE: PS01258; BH2; 1.
CC PROSITE: PS01259; BH3; 1.
CC PROSITE: PS01260; BH4.1; 1.
CC PROSITE: PS50063; BH4.2; 1.
CC Apoptosis; Transmembrane; Mitochondrion.
CC DOMAIN 10 30 BH4.
CC FT DOMAIN 87 101 BH3.
CC FT DOMAIN 130 149 BH1.
CC FT DOMAIN 181 196 BH2.
CC FT TRANSMEM 208 228 POTENTIAL.
CC FT CONFLICT 64 64 E -> S (IN REF. 2).
CC FT CONFLICT 67 82 GSAASEVPPAEGRLP -> ARLLVRCPLRGCA
CC CONFLICT 121 121 (IN REF. 2).
CC CONFLICT 139 139 H -> T (IN REF. 2).
CC CONFLICT 139 139 G -> V (IN REF. 2).
CC SQ SEQUENCE 233 AA; 25687 MW; 5252555ACB6E4C3D CRC64;

Query Match 16.6%; Score 183.5; DB 1; Length 233;
Best Local Similarity 26.9%; Pred. No. 2.2e-09;
Matches 57; Conservative 35; Mismatches 87; Indels 33; Gaps 10;

OY 2 ASGGS -GGPRQEGEGEALPSAEQVAQTEVEYFRSRYVYRHQOQDEAGVAAPADPE 59
DB 31 AAGEGRPPVP-----AA-PAAPAAVA-----AAGASSHRRPPEGSAASEVPA 77
OY 60 MVTPLQPSSTMGVYGLQRLAI--IGDDINRRYDSFEQTMQLHPTLTAENAYEFTKIATS 117
DB 78 EGLRAPR-----GVALLARQADESKRYQDFQMSQQLLPTTARGRVAAVEE 130
OY 118 LFESGINKGRVALLGEGYRLALNVYQGLNGFLGVQYTRFVYDMLHHCIARWIAQSGW 177
DB 131 LFRDGVNMGRIYAFEEFGVACVSVNREMSPLVDNITMTETVLNRR-LHNWITQDNGW 189
OY 178 VAALNL-GNG--PI-----LNVVLVGLVILG 201
DB 190 DAFVELYGNMRPLFDSSWISLKTLLSLVIG 221

RESULT 8
BCLX_MOUSE

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ID BCLX_MOUSE STANDARD: PRT; 233 AA.
AC 064373; 060557; 060558; 061338;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Apoptosis regulator Bcl-x.
DE BCL2L1 OR BCL2L OR BCLX.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2A4B;
RA Kamesaki H., Michaud G.Y., Takatsu K., Okuma M.;
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(BETA)).
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=95331139; PubMed=7607090;
RA Gonzalez-Garcia M., Perez-Ballester R., Ding L., Duan L., Boise L.H.,
RT Thompson C.B., Nunez G.;
RT "bcl-xL is the major bcl-x mRNA form expressed during murine
RT development and its product localizes to mitochondria.";
RL Development 120:3033-3042(1994).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS X(L); X(S) AND X(DELTA-TM)).
RC TISSUE=Pre-B cell;
RX MEDLINE=95052604; PubMed=7963517;
RA Fang W., Rivard J.-C., Mueller D.L., Behrens T.W.;
RT "Cloning and molecular characterization of mouse bcl-x in B and T
RT lymphocytes.";
RL J. Immunol. 153:4388-4398(1994).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM X(BETA)).
RC STRAIN=C57BL/6 X CBA; TISSUE=Thymus;
RX MEDLINE=98051053; PubMed=9390687;
RA Yang X.-F., Weber G.F., Cantor H.;
RT "A novel Bcl-x isoform connected to the T cell receptor regulates
RT apoptosis in T cells.";
RL Immunol. 7:629-639(1997).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=97289584; PubMed=9144489;
RA Grillot D.A., Gonzalez-Garcia M., Ekhterae D., Duan L., Inohara N.,
RT Ohta S., Seidman M.F., Nunez G.;
RT "Genomic organization, promoter region analysis, and chromosome
RT localization of the mouse bcl-x gene.";
RL J. Immunol. 158:4750-4757(1997).
CC -1- FUNCTION: Potent inhibitor of cell death. Inhibits activation of
CC caspases (By similarity). Appears to regulate cell death by
CC blocking the voltage-dependent anion channel (VMAC) by binding
CC to it and preventing the release of the caspase activator,
CC cytochrome c, from the mitochondrial membrane. The Bcl-x(S)
CC isoform promotes apoptosis.
CC -1- SUBUNIT: Bcl-x(L) forms heterodimers with BAX, BAK and Bcl-2 (By
CC similarity). Heterodimerization with BAX does not seem to be
CC required for anti-apoptotic activity (By similarity).
CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANE AND PERINUCLEAR
CC ENVELOPE FOR BCL-X(L). CYTOPLASMIC FOR BCL-X(DELTA-TM).
CC -1- ALTERNATIVE PRODUCTS: 4 ISOFORMS; BCL-X(L) (SHOWN HERE), BCL-X(S),
CC BCL-X(BETA) AND BCL-X(DELTA-TM); ARE PRODUCED BY ALTERNATIVE
CC SPLICING.
CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED, WITH HIGHEST LEVELS IN THE
CC BRAIN, THYMUS, BONE MARROW, AND KIDNEY. BCL-X(L) AND BCL-X(DELTA-
CC TM) EXPRESSION IS ENHANCED IN B AND T LYMPHOCYTES THAT HAVE BEEN
CC ACTIVATED.
CC -1- DEVELOPMENTAL STAGE: BCL-X(BETA) IS EXPRESSED IN BOTH EMBRYONAL AND
CC POSTNATAL TISSUES, WHEREAS BCL-X(L) IS PREDOMINANTLY FOUND IN
CC POSTNATAL TISSUES.
CC -1- DOMAIN: The BH4 domain is required for anti-apoptotic activity.
CC The BH1 and BH2 domains are required for both heterodimerization
CC with other Bcl2 family members and for repression of cell death.

```

CC -1- PM: Proteolytically cleaved by caspases during apoptosis (By
CC similarity). The cleaved protein, lacking the BH4 domain, has pro-
CC apoptotic activity (By similarity).
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X83574; CAA58557.1; -;
CC EMBL; L35049; AAA51039.1; -;
CC EMBL; L35048; AAA51040.1; -;
CC EMBL; U10102; AAA82174.1; -;
CC EMBL; U10101; AAA82173.1; -;
CC EMBL; U10100; AAA82172.1; -;
CC EMBL; 051279; AAC53460.1; -;
CC EMBL; 078031; AAB96881.1; -;
CC EMBL; 078030; AAB96881.1; JOINED.
CC HSSP; P53563; IAF3.
CC MGD; MGI:88139; Bcl2l.
CC InterPro; IPR002475; BCL2_family.
CC InterPro; IPR000712; BCL2_BH.
CC InterPro; IPR003093; BCL2_BH4.
CC InterPro; IPR004725; BCL2_reg.
CC Pfam; PF00452; BCL-2; 1.
CC Pfam; PF02180; BH4; 1.
CC SMART; SM00337; BCL; 1.
CC SMART; SM0265; BH4; 1.
CC TIGRFAMs; TIGR00865; bcl-2; 1.
DR PROSITE; PS50062; BCL2_FAMILY; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01258; BH2; 1.
DR PROSITE; PS01259; BH3; 1.
DR PROSITE; PS01260; BH4; 1.
DR PROSITE; PS50063; BH4_2; 1.
KW Apoptosis; Mitochondrion; Alternative splicing; Transmembrane.
FT DOMAIN 4 24 BH4.
FT DOMAIN 86 100 BH3.
FT DOMAIN 129 148 BH1.
FT DOMAIN 180 195 BH2.
FT TRANSMEM 210 226 POTENTIAL.
FT VARSPPLIC 126 188 MISSING (IN ISOFORM BCL-X(S)).
FT VARSPPLIC 189 233 DTFVLDYGNNAAESRKQERNNRWFLTGMTVAGVLLGSL
FT VARSPPLIC 194 233 FSRK -> VRTTPIVCPPLACVSLICEHP (IN ISOFORM
FT VARSPPLIC 194 233 BCL-X(BETA)).
FT VARSPPLIC 194 233 LYGNNAAESRKQERNNRWFLTGMTVAGVLLGSLFSRK
FT VARSPPLIC 194 233 -> GHDCMGCSAGLTIDSEVTRH (IN ISOFORM BCL-
FT VARSPPLIC 194 233 X(DELTA-1M)).
SQ SEQUENCE 233 AA; 26132 MW; 24D2AC798B7E072E CRC64;
Query Match 16.4%; Score 181; DB 1; Length 233;
Best Local Similarity 28.3%; Pred. No. 3; 7e-09;
Matches 43; Conservative 23; Mismatches 70; Indels 16; Gaps 3;

RESULT 9
BCLX_RAT STANDARD: PRT: 233 AA
ID BCLX_RAT P53563; Q62678; P70614; Q62836; Q64087; Q64128;
AC P53563; Q62678; P70614; Q62836; Q64087; Q64128;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Apoptosis regulator Bcl-x.
GN BCL2L OR BCL2L OR BCLX.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(S)).
RC TISSUE=Brain;
RA Michaelidis T.M.;
RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Wasselingh S.L., David G.L., Choi S., Velluona M., Hardwick J.M.;
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(BETA)).
RC TISSUE=Thymus;
RA MEDLINE=96278736; PubMed=8662675;
RX Shiraawa N., Inohara N., Okada S., Yuzaki M., Shoji S.-I., Ohta S.;
RT "An additional form of rat Bcl-x, Bcl-xbeta, generated by an
RT unspliced RNA, promotes apoptosis in promyeloid cells."
RL J. Biol. Chem. 271:13258-13265(1996).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(S)).
RC STRAIN=Sprague-Dawley; TISSUE=Ovary;
RX MEDLINE=95129487; PubMed=7828536;
RA Tilly J.L., Tilly K.I., Kenton M.L., Johnson A.L.;
RT "Expression of members of the Bcl-2 gene family in the immature rat
RT ovary: equine chorionic gonadotropin-mediated inhibition of granulosa
RT cell apoptosis is associated with decreased bax and constitutive
RT bcl-2 and bcl-xlong messenger ribonucleic acid levels."
RL Endocrinology 136:232-241(1995).
RN [5]
RX X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
RA MEDLINE=98010630; PubMed=9346936;
RA Arltomi M., Kunishima N., Inohara N., Ishibashi Y., Ohta S.,
RA Morikawa K.;
RT "Crystal structure of rat Bcl-xL. Implications for the function of
RT the Bcl-2 protein family."
RL J. Biol. Chem. 272:27886-27892(1997).
CC -1- FUNCTION: Potent inhibitor of cell death. Inhibits activation of
CC caspases (By similarity). Appears to regulate cell death by
CC blocking the voltage-dependent anion channel (VDAC) by binding
CC to it and preventing the release of the caspase activator,
CC cytochrome c, from the mitochondrial membrane. The Bcl-x(s) and
CC Bcl-x(beta) isoforms promote apoptosis.
CC -1- SUBUNIT: Bcl-x(L) forms heterodimers with BAX, BAK and Bcl-2 (By
CC similarity). Heterodimerization with BAX does not seem to be
CC required for anti-apoptotic activity (By similarity).
CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR
CC ENVELOPE (BY SIMILARITY).
CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS: BCL-X(L) (SHOWN HERE), BCL-X(S)
CC AND BCL-X(BETA); ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN MOST TISSUES. BCL-X(BETA) IS
CC SPECIFICALLY EXPRESSED IN CEREBELLUM, HEART, AND THYMUS. IN THE
CC OVARY, THE PREDOMINANT FORM IS BCL-X(L), WITH A SMALL BUT
CC DETECTABLE LEVEL OF BCL-X(S).
CC -1- DOMAIN: The BH4 domain is required for anti-apoptotic activity.
CC The BH1 and BH2 domains are required for both heterodimerization
CC with other Bcl2 family members and for repression of cell death.
CC -1- PM: Proteolytically cleaved by caspases during apoptosis. The
CC cleaved protein, lacking the BH4 domain, has pro-apoptotic

CC - FUNCTION: Suppresses apoptosis in a variety of cell systems.
 CC Including factor-dependent lymphohematopoietic and neural cells.
 CC Regulates cell death by controlling the mitochondrial membrane
 CC permeability. Appears to function in a feedback loop system with
 CC caspases. Inhibits caspase activity either by preventing the
 CC release of cytochrome c from the mitochondria and/or by binding to
 CC the apoptosis-activating factor (APAF-1).
 CC - SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and
 CC Bcl-x(L). Heterodimerization with BAX requires intact BH1 and BH2
 CC domains, and is necessary for anti-apoptotic activity (by
 CC similarity). Also interacts with APAF-1 and RAf-1.
 CC - SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular
 CC membrane of the nuclear envelope and the endoplasmic reticulum.
 CC - ALTERNATIVE PRODUCTS: 2 isoforms; alpha (shown here) and beta;
 CC are produced by alternative splicing.
 CC - TISSUE SPECIFICITY: Expressed in a variety of tissues.
 CC - DOMAIN: The BH4 domain is required for anti-apoptotic activity and
 CC for interaction with RAf-1.
 CC - PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2
 CC anti-apoptotic activity. Growth factor-stimulated phosphorylation
 CC on Ser-70 by PKC is required for the anti-apoptosis activity and
 CC occurs during the G2/M phase of the cell cycle. In the absence of
 CC growth factors, Bcl2 appears to be phosphorylated by other protein
 CC kinases such as ERKs and stress-activated kinases.
 CC - DEPHOSPHORYLATED BY: Protein phosphatase 2A (PP2A).
 CC - PTM: Proteolytically cleaved by caspases during apoptosis. The
 CC cleaved protein, lacking the BH4 domain, has pro-apoptotic
 CC activity, causes the release of cytochrome c into the cytosol
 CC promoting further caspase activity.
 CC - SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.
 CC - SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.
 CC - SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.
 CC - SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.
 CC - SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
 CC -----
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 CC -----
 DR EMBL: L31532; AAA37282.1; -
 DR EMBL: M16506; AAA37282.1; JOINED.
 DR EMBL: M16506; AAA37281.1; -
 DR PIR: A25960; TVMSA1.
 DR PIR: B25960; TVMSA1.
 DR PIR: E37332; E37332.
 DR HSP: Q07817; IMA2.
 DR MGI: 88138; Bcl2.
 DR InterPro: IPR002475; BCL2_family.
 DR InterPro: IPR000712; BCL2_BH.
 DR InterPro: IPR003093; Bcl2_BH4.
 DR InterPro: IPR004725; Bcl2_Reg.
 DR Pfam: PF00452; Bcl-2; 1.
 DR Pfam: PF02180; BH4; 1.
 DR SMART: SM00337; BCL; 1.
 DR SMART: SM00265; BH4; 1.
 DR TIGRfams: TIGR00865; bcl-2; 1.
 DR PROSITE: PS50062; BCL2_FAMILY; 1.
 DR PROSITE: PS01080; BH1; 1.
 DR PROSITE: PS01258; BH2; 1.
 DR PROSITE: PS01259; BH3; 1.
 DR PROSITE: PS01260; BH4; 1.
 DR PROSITE: PS01261; BH4_1; 1.
 DR PROSITE: PS50063; BH4_2; 1.
 DR Apoptosis; Alternative splicing; Transmembrane; Mitochondrion;
 DR Phosphorylation.
 FT DOMAIN 10 30 BH4
 FT DOMAIN 90 104 BH3
 FT DOMAIN 133 152 BH1
 FT DOMAIN 184 199 BH2
 FT TRANSMEM 209 230 POTENTIAL.

FT SITE 34 35
 FT MOD_RBS 70 70
 FT VARSPLIC 193 236
 FT SEQUENCE 236 AA; 26425 MW; AA85FE6B0766BDA CRC64;
 SO
 Query Match 16.38; Score 179.5; DB 1; Length 236;
 Best Local Similarity 24.4%; Pred. No. 5.1e-09;
 Matches 55; Conservative 31; Mismatches 92; Indels 47; Gaps 7;
 QY 22 ASEDVADDTREVRFRSYVEYRHOE-----QEAEEVAP--ADPEMTPLPDP--SSTMGV 74
 DB 2 AAGRTGTDNNEIYMKIITHYLSQRTGTEWDAGDAAPLGALPPGTFSPSPSPAPAV 61
 QY 75 GRGLAI-----IGDDINRRYSFEQTMLOHLPAAE 105
 DB 62 HREMAARTSLPLPLVATAGPALSPVPCVHLTLRRADDSPRRRNDFAFMSQSLHLP 121
 QY 106 NAYEYFKIKATSLFESGINSNGRYVALLFGYRLAHYQGLGQVTRFVYDEMHLH 165
 DB 122 TARGRFATVEELFRDGVNMGRIYAFEFEGVNCVESVNEKSPVDNLTMTETYLNRH 181
 QY 166 CIARMIARGGWVALNMGPI-----INVLVLGVLLG 201
 DB 182 -LHTWIDQNGGNAPFVL-VGSPMRPLFDPSWISIKTLISLALVG 224
 RESULT 12
 BCL2_RAT STANDARD; PRT; 236 AA.
 ID BCL2_RAT
 AC P49950; 062837; 064032;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Apoptosis regulator Bcl-2.
 GN BCL2 OR BCL-2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID-10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Brain;
 RX MEDLINE=94193015; PubMed=8144041;
 RA Sato T., Irie S., Krajewski S., Reed J.C.;
 RT "Cloning and sequencing of a cDNA encoding the rat Bcl-2 protein.";
 RL Gene 140:291-292(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Sprague-Dawley; TISSUE-Ovary;
 RX MEDLINE=95129487; PubMed=7828536;
 RA Tilly J.L., Tilly K.I., Kenton M.L., Johnson A.L.;
 RT "Expression of members of the bcl-2 gene family in the immature rat
 RT ovary: equine chorionic gonadotropin mediated inhibition of granulosa
 RT cell apoptosis is associated with decreased bax and constitutive
 RT bcl-2 and bcl-x(l) messenger ribonucleic acid levels.";
 RL Endocrinology 136:232-241(1995).
 RN [3]
 RP SEQUENCE OF 19-172 FROM N.A.
 RX MEDLINE=95059917; PubMed=7969891;
 RA Castren E., Onga Y., Berzaghi M.P., Tzimagiorgis G., Thoenen H.,
 RA Lindholm D.;
 RT "Bcl-2 messenger RNA is localized in neurons of the developing and
 RT adult rat brain.";
 RL Neuroscience 61:165-177(1994).
 CC - FUNCTION: Suppresses apoptosis in a variety of cell systems
 CC including factor-dependent lymphohematopoietic and neural cells.
 CC Regulates cell death by controlling the mitochondrial membrane
 CC permeability. Appears to function in a feedback loop system with
 CC caspases. Inhibits caspase activity either by preventing the
 CC release of cytochrome c from the mitochondria and/or by binding to
 CC the apoptosis-activating factor (APAF-1).
 CC - SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and

bcl-x(L). Heterodimerization with BAX requires intact BH1 and BH2 domains, and is necessary for anti-apoptotic activity (By similarity). Also interacts with APAF-1 and RAIF-1 (By similarity).

-1- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular membrane of the nuclear envelope and the endoplasmic reticulum.

-1- TISSUE SPECIFICITY: Expressed in a variety of tissues, with highest levels in reproductive tissues. In the adult brain, expression is localized in mitral cells of the olfactory bulb, granule and pyramidal neurons of hippocampus, pontine nuclei, cerebellar granule neurons, and in ependymal cells. In prenatal brain, expression is higher and localized in the neuroepithelium and in the cortical plate.

-1- DOMAIN: The BH4 domain is required for anti-apoptotic activity and for interaction with RAIF-1 (By similarity).

-1- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2 anti-apoptotic activity. Growth factor-stimulated phosphorylation on Ser-70 by PKC is required for the anti-apoptosis activity and occurs during the G2/M phase of the cell cycle. In the absence of growth factors, Bcl2 appears to be phosphorylated by other protein kinases such as ERKs and stress-activated kinases.

-1- PTM: Proteolytically cleaved by caspases during apoptosis. The cleaved protein, lacking the BH4 domain, has pro-apoptotic activity, causes the release of cytochrome c into the cytosol promoting further caspase activity (By similarity).

-1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.

-1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.

-1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.

-1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.

-1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.

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CC -----

DR EMBL: L14680; AAA53662.1; -

DR EMBL: U34964; AAA77687.1; -

DR EMBL: S74122; -; NOT_ANNOTATED_CDS.

DR HSSP: Q07817; IMA2.

DR InterPro: IPR002475; BCL2_family.

DR InterPro: IPR000712; BCL2_BH.

DR InterPro: IPR003093; BCL2_BH4.

DR InterPro: IPR004725; BCL2-reg.

DR Pfam: PF00452; BCL-2; 1.

DR Pfam: PF02180; BH4; 1.

DR SMART: SM00337; BCL; 1.

DR SMART: SM00265; BH4; 1.

DR TIGRFAMs: TIGR00865; bcl-2; 1.

DR PROSITE: PS50062; BCL2_FAMILY; 1.

DR PROSITE: PS01080; BH1; 1.

DR PROSITE: PS01258; BH2; 1.

DR PROSITE: PS01259; BH3; 1.

DR PROSITE: PS01260; BH4_1; 1.

DR PROSITE: PS50063; BH4_2; 1.

DR Apoptosis; Transmembrane; Mitochondrion; Phosphorylation.

KW DOMAIN 10 BH4.

FT DOMAIN 90 BH3.

FT DOMAIN 133 BH1.

FT DOMAIN 184 BH2.

FT TRASMEM 230 POTENTIAL.

FT SITE 34 CLEAVAGE (BY CASPASES) (BY SIMILARITY).

FT MOD_RES 70 A -> R (IN REF. 2).

FT CONFLICT 42 E -> G (IN REF. 1).

FT CONFLICT 157 S -> Y (IN REF. 2).

FT CONFLICT 164 L -> Q (IN REF. 2).

FT CONFLICT 212 L -> Q (IN REF. 2).

SO SEQUENCE 236 AA; 26622 MW; E7688CB9071A872A CRC64;

Query Match 16.2%; Score 178.5; DB 1; Length 236;

Best Local Similarity 24.2%; Pred. No. 6.2e-09; Matches 55; Conservative 31; Mismatches 90; Indels 51; Gaps 7;

QY 22 AAEEDVADTEEVFFSYFYRHQ-----DEAGGVAPA----- 56

DB 2 AAGRGYNRIKVIYTKLSQGYEMDQDEDSALPRAAPFGIRFPESNRPAV 61

QY 57 --DPEAVTLPLQSSMGVGRQLAI-----GDDINRRYDSEFQTMLOHLOPT 103

DB 62 HRDTARTSPLRP--LVNAGPALSPVPVYHLTLRRAGDFSRRYRRDFEMSQHLIT 119

QY 104 AENAYTFPKIATSFESGIMNGRVALLGFGYRLALHYQHLGFLGQYTRFVDFML 163

DB 120 PFTARGFATVVEELFRDGVNNGRIYAFEEFGVGVCSVNRKMSPLVDNIALMTETLN 179

QY 164 HHCIAWIAQGGWVAALNLGNPI-----INVLVLGVLLG 201

DB 180 RH-LHWIDNGMGDAFVEL-YGPSRPLPDEFSWLSLTLSIALVIG 224

RESULT 13

ID	BCIW_HUMAN	STANDARD:	PRT:	193 AA.
AC	Q92843:	01-NOV-1997 (rel. 35, Created)		
DT	01-NOV-1997 (rel. 35, Last sequence update)			
DI	15-JUN-2002 (rel. 41, Last annotation update)			
DE	Apoptosis regulator Bcl-w.			
GN	BCL2L2 OR BCLW OR KIAA0271.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=96358615; PubMed=8761287;			
RA	Gibson L., Holmgren S.P., Huang D.C., Bernard O., Copeland N.G.,			
RA	Jenkins N.A., Sutherland G.R., Baker E., Adams J.M., Cory S.,			
RT	"bcl-w, a novel member of the bcl-2 family, promotes cell survival.";			
RL	Oncogene 13:665-675(1996).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain;			
RX	MEDLINE=97191544; PubMed=9039502;			
RA	Nagase T., Seki N., Ishikawa K.-I., Ohira M., Kawarabayashi Y.,			
RA	Ohara O., Tanaka A., Kotani H., Miyajima N., Nomura N.,			
RT	"Prediction of the coding sequences of unidentified human genes. VI.			
RT	The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced by			
RT	analysis of cDNA clones from cell line K5-1 and brain.";			
RL	DNA Res. 3:321-328(1996).			
CC	-1- FUNCTION: PROMOTES CELL SURVIVAL.			
CC	-1- SUBCELLULAR LOCATION: Cytoplasmic.			
CC	-1- TISSUE SPECIFICITY: EXPRESSED IN ALMOST ALL MELOID CELL LINES AND			
CC	IN A WIDE RANGE OF TISSUES, WITH HIGHEST LEVELS IN BRAIN, COLON,			
CC	AND SALIVARY GLAND.			
CC	-1- DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC			
CC	FUNCTION.			
CC	-1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.			
CC	-1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.			
CC	-1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.			
CC	-1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL: U59747; AAB0905.1; -			
DR	EMBL: D87461; BAA19666.1; -			
DR	HSSP: Q07817; IMA2.			

DR Genew; HGNC:995; BCL2L2.
DR MIM; 601931; .
DR InterPro; IPR002475; BCL2_family.
DR InterPro; IPR000712; Bcl2_BH.
DR InterPro; IPR003093; Bcl2_BH4.
DR Pfam; PF00452; Bcl-2; 1.
DR SMART; PF02180; BH4; 1.
DR SMART; SM00337; BCL; 1.
DR SMART; SM00265; BH4; 1.
DR PROSITE; PSS0062; BCL2_FAMILY; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01258; BH2; 1.
DR PROSITE; PS01260; BH4_1; 1.
DR PROSITE; PSS0063; BH4_2; 1.
DR Apoptosis.
FT DOMAIN 9 29 BH4.
FT DOMAIN 85 104 BH1.
FT DOMAIN 136 151 BH2.
SQ SEQUENCE 193 AA; 20774 MW; 3792243A50281761 CRC64;

Query Match 16.0%; Score 176; DB 1; Length 193;
Best Local Similarity 28.2%; Pred. No. 8.1e-09;
Matches 57; Conservative 25; Mismatches 86; Indels 34; Gaps 6;

QY 28 AODEEVEFRSYVFRHCOE---QEAEGVAAAPDPEMTLPLQPSSTMGVGRQALITGD 83
DB 7 APTFRALVADPFGYKLRQKYVCGAGPGEPPADP-----LHQAMRAAGD 51
QY 84 DINRDSERFQTMLOHLOPTAENAYEFTKIATSLFESGINMGVVALFGYRLALHY 143
DB 52 EFERFRFRPSDLAQLHTVPSAQORFQVSELEFGSGPMNGRLVAFVFAALCAASV 111
QY 144 OHGLTGLGVTRFVVDPMHHCIARWIAORGCWV-----AALNIGNPIIYN 191
DB 112 NKEMEPIVGVGVGMWAV-LETRLADWISSSGMAEFALYGDALFEARRLREGMASV 170
QY 192 LVVL-GVLLGQFV-VRRFFKS 211
DB 171 RVLVTGAVAGALVTGAFAS 192

RESULT 14

BCLX_PIG STANDARD; PRT; 233 AA.
AC 077737;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Apoptosis regulator Bcl-x.
GN BCL2L1 OR BCL2L OR BCLX.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_Taxid=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-99171363; PubMed=10072723;
RA Bartling B., Hoffmann J., Holtz J., Schulz R., Heusch G., Darner D.;
RT "Quantification of cardioprotective gene expression in porcine
RT short-term hibernating myocardium".
RT J. Mol. Cell. Cardiol. 31:147-158(1999).
CC -!- FUNCTION: Potent inhibitor of cell death. Inhibits activation of
CC caspases (By similarity). Appears to regulate cell death by
CC blocking the voltage-dependent anion channel (VDAC) by binding
CC to it and preventing the release of the caspase activator,
CC cytochrome c, from the mitochondrial membrane.
CC -!- SUBUNIT: Bcl-x(L) forms heterodimers with BAX, BAK and Bcl-2 (By
CC similarity). Heterodimerization with BAX does not seem to be
CC required for anti-apoptotic activity (By similarity).
CC -!- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR
CC ENVELOPE (By similarity).
CC -!- DOMAIN: The BH4 domain is required for anti-apoptotic activity.
CC The BH1 and BH2 domains are required for both heterodimerization

CC with other Bcl2 family members and for repression of cell death.
CC -!- PTM: Proteolytically cleaved by caspases during apoptosis (By
CC similarity). The cleaved protein, lacking the BH4 domain, has pro-
CC apoptotic activity (By similarity).
CC -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.
CC -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----

DR EMBL; AJ001203; CAA04597.1; .
DR HSSP; Q07817; 1MA2.

DR InterPro; IPR002475; BCL2_family.
DR InterPro; IPR000712; Bcl2_BH.
DR InterPro; IPR003093; Bcl2_BH4.
DR InterPro; IPR004725; Bcl2_reg.
DR Pfam; PF00452; Bcl-2; 1.
DR Pfam; PF02180; BH4; 1.
DR SMART; SM00337; BCL; 1.
DR SMART; SM00265; BH4; 1.
DR TIGRFRAMS; TIGR00865; bcl-2; 1.
DR PROSITE; PSS0062; BCL2_FAMILY; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01258; BH2; 1.
DR PROSITE; PS01259; BH3; 1.
DR PROSITE; PS01260; BH4_1; 1.
DR PROSITE; PSS0063; BH4_2; 1.
DR Apoptosis; Mitochondrion; Transmembrane.
FT DOMAIN 4 24 BH4.
FT DOMAIN 86 100 BH3.
FT DOMAIN 129 148 BH1.
FT DOMAIN 180 195 BH2.
FT TRANSMEM 210 226
SQ SEQUENCE 233 AA; 26061 MW; 18BF6FA0441912B2 CRC64;

Query Match 16.0%; Score 176; DB 1; Length 233;
Best Local Similarity 27.6%; Pred. No. 1e-08;
Matches 42; Conservative 23; Mismatches 71; Indels 16; Gaps 3;

QY 71 MGQYGHQALITGDDINRRYDSFQTMLOHLOPTAENAYEFTKIATSLFESGINMGVVA 130
DB 83 MAAYVQALREAGDEFLRRRAFSDLTSQHLITPGTAYOSFEQVLELFRDGVNMGRIYA 142
QY 131 LGFGYRLALHYOHGLNGFVTRFVVDPMHHCIARWIAORGVVALN-GNCP-- 187
DB 143 FFSFGALCVESVDKEMQVLSRIATMAYTLNDH-LEPWIOENGMDTVVELYGNMAA 201
QY 188 -----ILNVLVVLGVLLGQFVVR 207
DB 202 ESRKQGERNNRFLTGMTIAGVLLGSLFSRK 233

RESULT 15

ARL1_XENLA STANDARD; PRT; 204 AA.
AC 091828;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Apoptosis regulator R11 (XRL1).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodidae; Xenopus.
OX NCBI_Taxid=8355;

```

RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Head;
RA MEDLINE-9531613; PubMed-7607538;
RX Cruz-Reyes J., Tata J.R.;
RT "Cloning, characterization and expression of two Xenopus bcl-2-like
   cell-survival genes.";
RL Gene 158:171-179(1995).
CC -1- FUNCTION: CONFERS STRONG PROTECTION AGAINST CELL DEATH.
CC -1- SUBCELLULAR LOCATION: Membrane-bound (Potential).
CC -1- DEVELOPMENTAL STAGE: DEVELOPMENTAL REGULATION ONLY OCCURS IN THE
CC BRAIN OF MID-METAMORPHOSIC TO POST-METAMORPHOSIC TADPOLES AND
CC ADULTS, WHERE AN INCREASE OF SEVERAL FOLD HAS BEEN OBSERVED.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
-----
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-----
CC EMBL; X82461; CNA57844.1; -.
DR HSSP; Q07817; IMAZ.
DR InterPro; IPR002475; BCL2_family.
DR InterPro; IPR000712; Bcl2_BH.
DR InterPro; IPR003093; Bcl2_BH4.
DR InterPro; IPR004725; Bcl2-reg.
DR Pfam; PF00452; Bcl-2; 1.
DR Pfam; PF02180; BH4; 1.
DR SMART; SM00337; BCL; 1.
DR SMART; SM00265; BH4; 1.
DR TIGRFAMs; TIGR00865; bcl-2; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01258; BH2; 1.
DR PROSITE; PS50062; BCL2_FAMILY; 1.
DR Apoptosis; Transmembrane.
KW DOMAIN
FT 101 120 BH1.
FT DOMAIN 152 167 BH2.
FT TRANSMEM 181 198 POTENTIAL.
SQ SEQUENCE 204 AA; 23379 MW; 3BFC6BE6DDA4CA03 CRC64;

Query Match 15.6%; Score 172.5; DB 1; Length 204;
Best Local Similarity 24.9%; Pred. NO. 1.8e-08;
Matches 44; Conservative 35; Mismatches 71; Indels 27; Gaps 4;

QY 57 DEPWTLPIQPS-----STMG---QVGRQALIIDDDINRRYDSEFQTMLOHQP7A 104
DB 29 NRPMPMYLMEPSTSRPGGATGIVEEYVLOALLEATEEFELRYORAFSDITSOLHITQ 88
QY 105 ENAYEYETKIAATSLPESGIMGGRVVALLGFGYRLAHYQGLGTFGQVTRFYVDMLH 164
DB 89 DTAQSQSQVQVMELEFRDGTNGRIYAFPSFGALCVESANKEMTDLPRIYQMVNY-LE 147
QY 165 HCLARWIAORGWVAALNIGN-----GPIINVLVVLGVVLLGQFVVR 207
DB 148 HTIQPMQENGWEAFVGLYKNAANAQSRSEGRGRLLTIVMLTGVALVCYMR 204

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Search completed: March 27, 2003, 10:52:49
 Job time : 15 secs


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      118 59 DNLSLEPNSVILGQVROLALIGDDINRRYDTERQNLLEQLPTAGNAYELFTKIASLSEK
      119 121 SGINMGKRVYALLGFGRALAHVYQHLGFLGQVTRFVYDDEMIHNCIARIKRGQGVAA
      120 119 SGISMRVYVALLGFGRALAHVYQRLTGFLGQVTCFLADIIILHVIARIWIRGQGVAA
      121 181 LINGNSPILNVLVGLVGLLQGFVVRFRPKS 211
      122 179 LSLRROPILSVYVIFGVVLLGQFVVRFRPRS 209

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RESULT 2

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      123 09MZS6 PRELIMINARY: PRT; 163 AA.
      124 09MZS6:
      125 01-OCT-2000 (Tremblrel, 15, Created)
      126 01-OCT-2000 (Tremblrel, 15, Last sequence update)
      127 01-JUN-2002 (Tremblrel, 21, Last annotation update)
      128 DE Bak protein (Fragment).
      129 OS Ovis aries (Sheep).
      130 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
      131 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
      132 Bovidae; Caprinae; Ovis.
      133 NCBI_TaxID=9940;
      134 [1]
      135 SEQUENCE FROM N.A.
      136 RP TISSUE-Ovary;
      137 RA Murray J.F., Dong Y.B., Leigh A.J., Scaramuzzi R.J., Carter N.D.;
      138 RT "Bak in the sheep ovary."
      139 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
      140 DR EMBL; AF164518; AAF89533.1; -.
      141 DR HSSP; Q16611; 1BXL.
      142 DR InterPro; IPR000712; BCL2_BH.
      143 DR InterPro; IPR002475; BCL2_family.
      144 DR Pfam; PF00452; BCL-2; 1.
      145 DR SMART; SM00337; BCL; 1.
      146 DR PROSITE; PS50062; BCL2_FAMILY; 1.
      147 DR PROSITE; PS01080; BH1; 1.
      148 DR PROSITE; PS01258; BH2; 1.
      149 DR PROSITE; PS01259; BH3; 1.
      150 FT NON_TER 1
      151 FT NON_TER 163
      152 SQ SEQUENCE 163 AA; 18039 MW; FB35EA8A8C53AD5B CRC64;

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      153 Query Match 66.5%; Score 733; DB 6; Length 163;
      154 Best Local Similarity 85.9%; Pred. No. 7.1e-63;
      155 Matches 140; Conservative 9; Mismatches 14; Indels 0; Gaps 0;

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      156 QY 42 RHQOEDAEAGVAPADPEWVTLPLQPSSTMGVGRQLALIGDDINRRYDSEFQTMQLQHLQ 101
      157 1 RHQOEDAEAGVAPADPEWVTLPLQPSSTMGVGRQLALIGDDINRRYDSEFQTMQLQHLQ 60
      158 DB 102 PTAENAYEYFTKATSLFESGIMWGRVYVALLGFGRALAHVYQHLGFLGQVTRVYDF 161
      159 61 PTAENAYEYFTKATSLFESGIMWGRVYVALLGFGRALAHVYQHLGFLGQVTRVYDF 120
      160 QY 162 MLHHCIARIWIRGQGVYVALLNGNPIILNVLVGLVGLLQGFV 204
      161 121 VLRRSTARIWIRGQGVYVALLNGNPIILNVLVGLVGLLQGFV 163
      162 DB

```

RESULT 3

```

      163 091MX5 PRELIMINARY: PRT; 151 AA.
      164 091MX5:
      165 01-DEC-2001 (Tremblrel, 19, Created)
      166 01-DEC-2001 (Tremblrel, 19, Last sequence update)
      167 01-JUN-2002 (Tremblrel, 21, Last annotation update)
      168 DE N-BAK1.
      169 GN BAK1.
      170 OS Mus musculus (Mouse).
      171 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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      172 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
      173 OX NCBI_TaxID=10090;
      174 [1]
      175 RP SEQUENCE FROM N.A.
      176 RC STRAIN=NMRI; TISSUE=NEURONAL;
      177 RX MEDLINE=21238300; PubMed=11278671;
      178 RA Sun Y.F., Yu L.Y., Saarna M., Timmusk T., Arumae U.;
      179 RT "Neuron-specific Bcl-2 homolog 3 domain-only splice variant of Bak is
      180 anti-apoptotic in neurons, but pro-apoptotic in non-neuronal cells.";
      181 RL J. Biol. Chem. 276:16240-16247(2001).
      182 DR EMBL; AF402617; AAL01876.1; -.
      183 DR InterPro; IPR000712; BCL2_BH.
      184 DR InterPro; IPR002475; BCL2_family.
      185 DR Pfam; PF00452; BCL-2; 1.
      186 DR PROSITE; PS50062; BCL2_FAMILY; 1.
      187 DR PROSITE; PS01259; BH3; UNKNOWN.1
      188 SQ SEQUENCE 151 AA; 16402 MW; 18C13BFF86E4F33B CRC64;

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      189 Query Match 41.0%; Score 452; DB 11; Length 151;
      190 Best Local Similarity 75.0%; Pred. No. 8.5e-36;
      191 Matches 87; Conservative 12; Mismatches 15; Indels 2; Gaps 1;

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      192 QY 1 MASGGPPPPROEGCEPALPSASEQVAQDTVEYFRSTYTRHQOEDAEAGVAPADPEM 60
      193 DB 1 MASGGPPPPRVGCDGS--PSPSEQVAQDTVEYFRSTYTRHQOEDAEAGVAPADPEM 58
      194 QY 61 VTLPLQPSSTMGVGRQLALIGDDINRRYDSEFQTMQLQHLQPTAENAYEYFTKAT 116
      195 DB 59 DNLSLEPNSVILGQVROLALIGDDINRRYDTERQNLLEQLPTAGNAYELFTKIAS 114

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RESULT 4

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      196 077738 PRELIMINARY: PRT; 80 AA.
      197 077738:
      198 01-NOV-1998 (Tremblrel, 08, Created)
      199 01-NOV-1998 (Tremblrel, 08, Last sequence update)
      200 01-JUN-2002 (Tremblrel, 21, Last annotation update)
      201 DE Bak protein (Fragment).
      202 GN BAK.
      203 OS Sus scrofa (Pig).
      204 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
      205 Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
      206 OX NCBI_TaxID=9823;
      207 [1]
      208 RP SEQUENCE FROM N.A.
      209 RA Bartling B., Hoffmann J., Holtz J., Schulz R., Heusch G., Darmer D.;
      210 RT "Expression of apoptosis-associated genes in hibernating and stunned
      211 myocardium of pig."
      212 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
      213 DR EMBL; AJ001204; CAA04598.1; -.
      214 DR HSSP; Q16611; 1BXL.
      215 DR InterPro; IPR000712; BCL2_BH.
      216 DR InterPro; IPR002475; BCL2_family.
      217 DR Pfam; PF00452; BCL-2; 1.
      218 DR SMART; SM00337; BCL; 1.
      219 DR PROSITE; PS50062; BCL2_FAMILY; 1.
      220 DR PROSITE; PS01259; BH3; 1.
      221 FT NON_TER 1
      222 FT NON_TER 80
      223 SQ SEQUENCE 80 AA; 8818 MW; FDIAF83BD7D59C86 CRC64;

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      224 Query Match 35.4%; Score 390; DB 6; Length 80;
      225 Best Local Similarity 92.5%; Pred. No. 3.4e-30;
      226 Matches 74; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

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      227 QY 50 EGVAAPADPEWVTLPLQPSSTMGVGRQLALIGDDINRRYDSEFQTMQLQHLQPTAENAYE 109
      228 DB 1 DGAAPADPEWVTLPLQPSSTMGVGRQLALIGDDINRRYDSEFQTMQLQHLQPTAENAYE 60
      229 QY 110 YFTKATSLFESGIMWGRV 129
      230 DB 61 YFTKATSLFESGIMWGRV 80

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RESULT 5
09M6F1 PRELIMINARY; PRT; 211 AA.
ID 09M6F1;
AC 09M6F1;
DT 01-NOV-1999 (Tremblrel. 12, Created)
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
DE 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Myeloid cell leukemia protein MCL-1 (Fragment).
OS Gallus gallus (Chicken)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99190706; PubMed=10090728;
RA Lee R.M., Gillet G., Burnside J., Thomas S.J., Neiman P.;
RT "Role of Nr13 in regulation of programmed cell death in the bursa of
RT Fabricius."
RL Genes Dev. 13:718-728(1999).
[2]
RP SEQUENCE FROM N.A.
RA Sofer L., Burnside J.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF120210; AAD31644.1; -.
DR InterPro; IPR000712; Bcl2_BH.
DR InterPro; IPR002475; Bcl2_family.
DR Pfam; PF00452; Bcl-2; 1.
DR SMART; SM00337; BCL; 1.
DR PROSITE; PS50062; BCL2_FAMILY; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01258; BH2; 1.
DR NON_TER 1
FT SEQUENCE 211 AA; 23143 MW; AAB057C63F92BAC7 CRC64;

Query Match
Best Local Similarity 16.4%; Score 181; DB 13; Length 211;
Matches 59; Conservative 44; Mismatches 81; Indels 40; Gaps 10;

OY 7 GCGPRGCGEPALPSASEOYAOPTEEVFRSYVYRHQOEOEAGVAAPA---DEPMVT 62
DB 4 PCTP-----PELPDLRIDELROESELILKYL-----REAGGEPEGVKKLPEGLG 50
OY 63 LPLOP-----SSTMGOVQOLAIIDDDINRRYDSEFQTMLOHPTAENAYEFTKIATSL 118
DB 51 GCGRGRASSAVMERKALETLRRVGDGVQKHELAFOGKLRLKLEIKKEDDLOANCEVAQV 110
OY 119 FESGI-NMGRVVALTGFGYRLAHV---YOHGLTGLGOVTRVVDPMHLHCIAIRIAQ 173
DB 111 FNDGYTNMGRVYTLISFGAFYAKHLKKSINDKCTSLAGITTAIVSSK-----REWLMS 165
OY 174 RGVVAALNLG-----NGPILNLVLVL-GVVLG---QFVVR 208
DB 166 OGWEGEVDFFRVEDLESSINVLMAFAGVAGLGSALAYMIRKX 209

RESULT 6
09N35 PRELIMINARY; PRT; 217 AA.
ID 09N35;
AC 09N35;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DE 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE B-cell leukemia/lymphoma x (Fragment).
GN BCLX.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

```

```

RC STRAIN-129/SVJ;
RA Yang X.-F., Cantor H.;
RT "Novel cDNA structure and genomic organization of apoptosis regulatory
RT gene Bcl-x-gamma."
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF133282; AAK15455.1; -.
DR EMBL; AF133281; AAK15455.1; JOINED.
DR HSSP; P53563; IAF3.
DR InterPro; IPR000712; Bcl2_BH.
DR InterPro; IPR002475; BCL2_FAMILY.
DR Pfam; PF00452; Bcl-2; 1.
DR SMART; SM00337; BCL; 1.
DR TIGRFAMs; TIGR00865; bcl-2; 1.
DR PROSITE; PS50062; BCL2_FAMILY; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01258; BH2; 1.
DR PROSITE; PS01259; BH3; 1.
DR NON_TER 1
FT SEQUENCE 217 AA; 24234 MW; 3B5A4E809A7DEF18 CRC64;

Query Match
Best Local Similarity 16.4%; Score 181; DB 11; Length 217;
Matches 43; Conservative 23; Mismatches 70; Indels 16; Gaps 3;

OY 71 MGCVGQOLAIIDDDINRRYDSEFQTMLOHPTAENAYEFTKIATSLFESGINMGHVA 130
DB 67 MAAYKQALREADDEFELRRAFSDLTSQLHTPOTAVQSEGVVNELEFRDGVWGKIVA 126
OY 131 LGFGYRLAHVYOHGLTGLGOVTRVVDPMHLHCIAIRIAQGGVVAALNL-GNCP-- 187
DB 127 FFSFGALCVESVDKEMOVLVSRISAWATYLNH-LEPMWIOENGWDVTDVLYGNNA 185
OY 188 -----ILNVLVVLGVVLGQFVVR 207
DB 186 ESRKQGERENRWFILGMTVAGVILGLSFSRK 217

RESULT 7
09MYW4 PRELIMINARY; PRT; 233 AA.
ID 09MYW4;
AC 09MYW4;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DE 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Bcl-X.
OS Oryctolagus cuniculus (Rabbit).
OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Eukaryota; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RA Knott J.C., Robertson L., James E.R.;
RT "Rabbit Bcl-X."
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY005131; AAF88137.1; -.
DR HSSP; P53563; IAF3.
DR InterPro; IPR000712; Bcl2_BH.
DR InterPro; IPR003093; BCL2_BH4.
DR InterPro; IPR002475; BCL2_FAMILY.
DR InterPro; IPR004725; Bcl2_reg.
DR Pfam; PF00452; Bcl-2; 1.
DR SMART; SM00337; BCL; 1.
DR SMART; SM00265; BH4; 1.
DR TIGRFAMs; TIGR00865; bcl-2; 1.
DR PROSITE; PS50062; BCL2_FAMILY; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01258; BH2; 1.
DR PROSITE; PS01259; BH3; 1.
DR PROSITE; PS01260; BH4.1; 1.
DR PROSITE; PS50063; BH4.2; 1.
DR NON_TER 1
FT SEQUENCE 233 AA; 25986 MW; 12F0F30344D53F93 CRC64;

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RA Nagafuchi S., Sano J., Kano R., Hasegawa A.;
 RT Molecular cloning of feline Bcl-2 family";
 RL Submitted (MAR-2002) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AB080951; BAB85856.2; -
 SQ SEQUENCE 233 AA; 26017 MW; CD17F24FE9DA7BC9 CRC64;

Query Match 16.3%; Score 180; DB 6; Length 233;
 Best Local Similarity 28.3%; Pred. No. 2,7e-09;
 Matches 43; Conservative 22; Mismatches 71; Indels 16; Gaps 3;

OY 71 MGVGROLAIIGDDINRRYSEFQTMLOHPTAENAYEFTKATSLFESGINMGHVA 130
 DB 83 MAAVKQALREADEDEFELRRRAFSQTSQTLHTPGTAYQSEGYVNEFRDGVNMGRIYA 142
 OY 131 LIGFGYRLALHYOGLTGFQGVYRVVDFMLHHCICARWIAQSGVVAALNT-GNCP-- 187
 DB 143 FFSFGALCVESVDKEMOVLRSIATAMATYLNH-LEPMIOENGWDTEVEYLGNNAAA 201
 OY 188 -----ILNVLVVGLVYLIGQFVVR 207
 DB 202 ESRKQERSNRWFLTGMVAGVLLGSLFSRK 233

RESULT 11

OY23R6 PRELIMINARY; PRT; 236 AA.
 AC OY23R6:
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE B-cell lymphoma protein 2.
 GN BCL2.
 OS Cricetus longicaudatus (Long-tailed hamster) (Chinese hamster).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Cricetus.
 OX NCBI_TaxID=10030;
 RN [1]
 RE SEQUENCE FROM N.A.
 RA Lai D.Z., Chen W., Mang H.T.;
 RT "Construction of a robust CHO cell line for biopharmaceutical use";
 RL Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AF04339; AAK92201.1; -
 DR InterPro: IPR000712; Bcl2_BH.
 DR InterPro: IPR003093; Bcl2_BH4.
 DR InterPro: IPR002475; Bcl2_family.
 DR InterPro: IPR004725; Bcl2_reg.
 DR Pfam: PF00452; Bcl-2; 1.
 DR Pfam: PF02180; BH4; 1.
 DR TIGRFAMS: TIGR00865; bcl-2; 1.
 DR PROSITE: PS50062; BCL2_FAMILY; 1.
 DR PROSITE: PS01080; BH1; UNKNOWN.1.
 DR PROSITE: PS01258; BH2; UNKNOWN.1.
 DR PROSITE: PS01259; BH3; UNKNOWN.1.
 DR PROSITE: PS01260; BH4.1; UNKNOWN.1.
 DR PROSITE: PS50063; BH4-2; 1.
 SQ SEQUENCE 236 AA; 26500 MW; BBDFO52EF32CA8B8 CRC64;

Query Match 16.1%; Score 177.5; DB 11; Length 236;
 Best Local Similarity 23.9%; Pred. No. 4,9e-09;
 Matches 56; Conservative 31; Mismatches 94; Indels 53; Gaps 7;

OY 22 AASEQVADTEVEFRSYVYRHOQ-----EAGVAPA- 56
 DB 2 AAGRTGDNREIVAKTHYKLSQRCYEMDGDVAAPLGAAPPGIFSQPSNPAPV 61
 OY 57 --DPEWTLPLQ-SSINGO-----VGRQLAIIGDDINRRYSEFQTMLOHPTAE 105
 DB 62 HRDMAARTSLPRPIATATGTPSPVPHLTLRADDSSKRYKRFAMSSQLHLPF 121
 OY 106 NAYEFTFIATSLFESGINMGHVAALIGFYRLALHYOGLTGFQGVYRVVDFMLAH 165
 DB 122 TARGRFATVEELFRDGVNMGRIYAFEFEGVNCVESVNRMSPLVDNALMWTETLNH 181

OY 166 CIARWIAQSGVVAALNLGNP-----ILNVLVVGLVYLIGQFV 204
 DB 182 -LHTWLDNGWDVAFVEL-YGVSVPRLDFDSWLSLXTLLNLALVAGACITLGTYL 233

RESULT 12

OY9NIA2 PRELIMINARY; PRT; 233 AA.
 AC OY9NIA2:
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Anti-apoptotic regulator Bcl-XL.
 GN BCL-XL.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RE SEQUENCE FROM N.A.
 RA TISSUE=HEART;
 RA Lee T.L., Canty J.M.;
 RT "PCR Cloning of a Porcine bcl-xL cDNA from Heart";
 RL Submitted (DEC-1999) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AF216205; AAF33212.1; -
 DR HSPB; Q07817; IMA2.
 DR InterPro: IPR000712; Bcl2_BH.
 DR InterPro: IPR003093; Bcl2_BH4.
 DR InterPro: IPR002475; Bcl2_family.
 DR InterPro: IPR004725; Bcl2_reg.
 DR Pfam: PF00452; Bcl-2; 1.
 DR Pfam: PF02180; BH4; 1.
 DR SMART: SM00337; BCL; 1.
 DR SMART: SM00265; BH4; 1.
 DR TIGRFAMS: TIGR00865; bcl-2; 1.
 DR PROSITE: PS50062; BCL2_FAMILY; 1.
 DR PROSITE: PS01080; BH1; 1.
 DR PROSITE: PS01258; BH2; 1.
 DR PROSITE: PS01259; BH3; 1.
 DR PROSITE: PS01260; BH4-1; 1.
 DR PROSITE: PS50063; BH4-2; 1.
 SQ SEQUENCE 233 AA; 26047 MW; 2FA312818B25E17D CRC64;

Query Match 16.0%; Score 177; DB 6; Length 233;
 Best Local Similarity 27.6%; Pred. No. 5,3e-09;
 Matches 42; Conservative 23; Mismatches 71; Indels 16; Gaps 3;

OY 71 MGVGROLAIIGDDINRRYSEFQTMLOHPTAENAYEFTKATSLFESGINMGHVA 130
 DB 83 MAAVKQALREADEDEFELRRRAFSQTSQTLHTPGTAYQSEGYVNEFRDGVNMGRIYA 142
 OY 131 LIGFGYRLALHYOGLTGFQGVYRVVDFMLHHCICARWIAQSGVVAALNT-GNCP-- 187
 DB 143 FFSFGALCVESVDKEMOVLRSIATAMATYLNH-LEPMIOENGWDTEVEYLGNNAAA 201
 OY 188 -----ILNVLVVGLVYLIGQFVVR 207
 DB 202 ESRKQERSNRWFLTGMVAGVLLGSLFSRK 233

RESULT 13

OY9BDD5 PRELIMINARY; PRT; 180 AA.
 AC OY9BDD5:
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Anti-apoptotic regulator Bcl-XL (Fragment).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
 OC Bovidae; Bovinae; Bos.

SEQ	09BIDX	PRELIMINARY;	PRT;	180 AA.
AC	09BIDX;			
DT	01-JUN-2001 (TREMBL;rel. 17, Created)			
DT	01-JUN-2001 (TREMBL;rel. 17, Last sequence update)			
DT	01-JUN-2002 (TREMBL;rel. 21, Last annotation update)			
DE	Anti-apoptotic regulator Bcl-xL (Fragment).			
OS	Bos taurus (Bovine).			
OC	Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidae;			
OC	Bovidae; Bovinae; Bos.			
OX	NCBI_TaxID=9913;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Amils M., Bouzat J.;			
RT	Characterization of the bovine bcl-xL gene and related pseudogenes. "			
RL	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AF245487; AAK31306.1; -			
DR	HSP; Q07817; IMAZ.			
DR	InterPro; IPR000712; BCL2_BH.			
DR	InterPro; IPR002475; BCL2_family.			
DR	Pfam; PF00452; BCL-2; 1.			
DR	SMART; SM00337; BCL; 1.			
DR	PROSITE; PS50062; BCL2_FAMILY; 1.			
DR	PROSITE; PS01258; BH2; 1.			
DR	PROSITE; PS01259; BH3; 1.			
FT	NON_TER 1			
FT	NON_TER 180			
FT	NON_TER 180			
SEQ	SEQUENCE	180 AA;	20056 MW;	62C4C0BD055A95F CRC64;

Query Match	15.88;	Score 174;	DB 6;	Length 180;
Best Local Similarity	28.8%;	Pred. No. 7.3e-09;		
Matches 42;	Conservative 21;	Mismatches 67;	Indels 16;	Gaps 3

RESULT	ID	PRELIMINARY	PRT	193 AA.
088996				
ID	088996			
AC	088996			
DT	01-NOV-1998	(TREMBLrel_08, Created)		
DT	01-NOV-1998	(Last sequence update)		
DT	01-JUN-2002	(TREMBLrel_21, Last annotation update)		
DE	Bcl-1.			
GN	BCL-1.			
OS	Rattus norvegicus (Rat).			
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OC				
OX	NCBI_TaxID=10116;			
RN	[1]			
RC	SEQUENCE FROM N.A.			
RC	STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN;			
RX	MEDLINE=99292146; PubMed=10366024;			
RA	Hamner S., Skoglosa Y., Lindholm D.,			
RT	"Differential expression of bcl-1 and bcl-2 messenger RNA in the			
RL	developing and adult rat nervous system.";			
RL	Neuroscience 91:673-684(1999).			
RL	EMBL: AF096291; AAC64200.1; .			
DR	HSSP: 007817; 1MAZ.			
DR	InterPro: IPR000712; Bcl2_BH.			
DR	InterPro: IPR003093; Bcl2_BH4.			
DR	InterPro: IPR002475; Bcl2_family.			
DR	Pfam: PF00452; Bcl-2; 1.			
DR	Pfam: PF00452; Bcl-2; 1.			
DR	SMART: SM00337; BCL; 1.			
DR	SMART: SM00265; BH4; 1.			
DR	PROSITE: PS00622; BCL2_FAMILY; 1.			
DR	PROSITE: PS01080; BH1; 1.			
DR	PROSITE: PS01258; BH2; 1.			
DR	PROSITE: PS01260; BH4_1; 1.			
DR	PROSITE: PS00063; BH4_2; 1.			
SO	SEQUENCE 193 AA; 20820 MW; 36D6742F529AFB4 CRC64;			

	Query Match	15.6%	Score 172	DB 11	Length 193	
	Best Local Similarity	28.0%	Pred. No. 1,36-08			
	Matches	56	Conservative	25	Mismatches	85
					Indels	34
					Gaps	6
Oy	30	DTEEVSRYFYRHOQE---	QEAEGVAAPADPEKWTLP	LLOPSSTMQVGRQLAII	GGDI	85
		: : : : :		: : : : :		
Db	9	DTRLALVADFYGLTKRQKGYVCGACGDEGPAADP			LHOAMRAAGDEF	53
Oy	86	NRKRDSEFQIMLQHLP	ENAYETTKATSLFESG	INMGVYALLGFG	TRLALHYOH	145
		: : : : :	: : : : :	: : : : :		
Db	54	ETRRRTFSDLAQLAHVT	PESQAQRTQVSDLE	FGGGRNMGLVAF	VEFGALCAESVNK	113
Oy	146	GLTEFLGQVTRFYVDENL	HHICIRMTAQRGVN			
		: : : : :	: : : : :			
Db	114	EMEPVVGQVQDDMVVTV	-LETRLDMDTHSSGGA	NEFTALYGDGAL	EEARRRLREGMMASVKT	172
Oy	194	VL-GVYLLGQV-VRREFS	211			
		: : : : :	: : : : :			
Db	173	VLTGAVALGALVYGAFFAS	192			

Search completed: March 27, 2003, 10:53:27
Job time : 32 secs